**FIG. 1A**

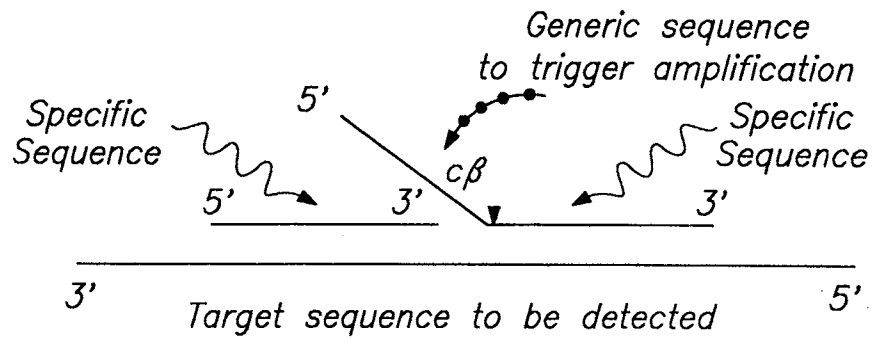
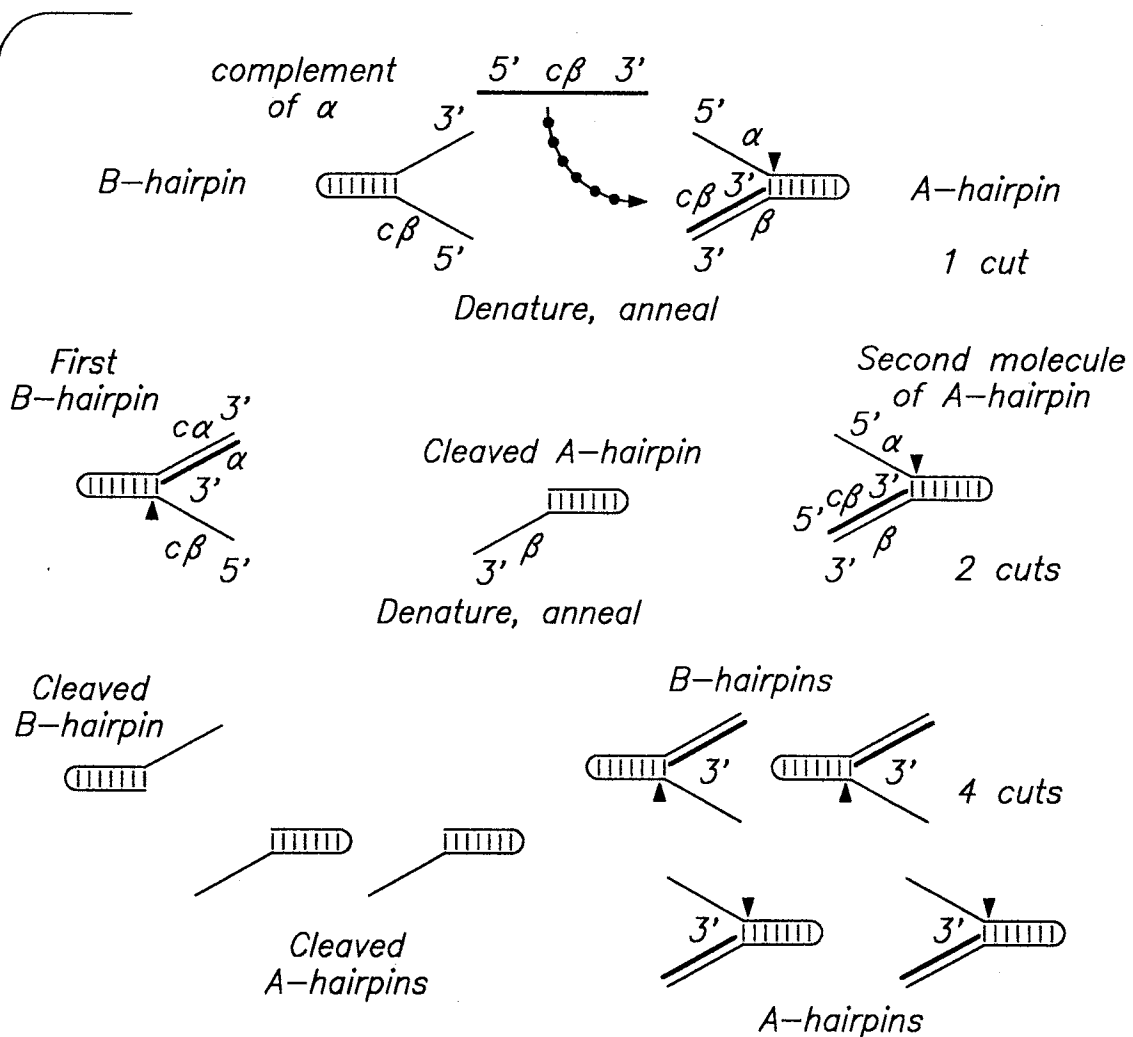
FIG. 1B**PART ONE: TRIGGER REACTION****PART TWO: DETECTION REACTION**

FIG. 2A

```

MAJORITY [SEQ ID NO:7]  ATGXXGGCGATGCTTCCGCTCTTTGAGCCCAAGGGCGGCTCCTCCTGGTGGAGCGGCCACGACCTGGCCT
DNAPTAQ [SEQ ID NO:1]  ... AG..G.....G.....G..... 70
DNAPTFL [SEQ ID NO:2]  ... ..C.....C..G..... 67
DNAPTTH [SEQ ID NO:3]  ... GA.....G.....A..... 70

MAJORITY  ACGGCACCTTCTTGGGCTGAAGGGCTCAGCACCGCGGGGGGAACGGGTGCAGGGGCTCTACGGCTT

DNAPTAQ  .....CA.....G.....G..... 140
DNAPTFL  .....T.....C.....G.....C..T..... 137
DNAPTTH  .....G.....G..... 140

MAJORITY  CGCCAAAGAGCGCTCCTCAAGGGCTGAAGGAGGAGCGGGGACXXGGGGGTGXTGGTCTTTGACGCCAAG

DNAPTAQ  .....G.....A..... 207
DNAPTFL  .....A.....GT..T..... 204
DNAPTTH  .....T.....T..AA...C..GT..... 210

MAJORITY  GCGCCCTCCTTCCGGCCACGAGGGCTACGAGGCTACAAGCGGGCGGGCCCGCCAGCGCGGAGGACTTTC

DNAPTAQ  .....G..GG.....G..... 277
DNAPTFL  ..... 274
DNAPTTH  .....GA.....G.....C.....C. 280

MAJORITY  CCGGGCAGCTCGGCTCATCAAGGAGCTGGTGGACCTCCTGGGCTTGGGGGCTCGAGGTCCCCGGCTA

DNAPTAQ  .....A.....G.....G.....G..... 347
DNAPTFL  .....G.....T.....A..C....T...G..G....T.....T 344
DNAPTTH  .....T.....T..A..C..... 350

```

FIG. 2B

MAJORITY [SEQ ID NO:73]	CGAGGGGGACGACGTXCTGGCCACCCTGGCCCAAGAAAGGGGCAAAAGGAGGGGTACGAGGTCGGGCATCCTC	
DNAPTAQ [SEQ ID NO:1]C.....G.....C.....C.....C.....	417
DNAPTFL [SEQ ID NO:2]	T.....G.....CG.....	414
DNAPTTH [SEQ ID NO:3]T..G.....	420
MAJORITY	ACGGCGGACGGGACCTCTACGAGTCCTTTCGGAGCGGCATGCCCGTCCTCCACCCGCGAGGGGTAGCTCA	
DNAPTAQAAA.....T.....CA.....	487
DNAPTFL	T.....G.....G.....A.....T.....G.....	484
DNAPTTHA..G.G.....G.....GG.....	490
MAJORITY	TCACCCCGGGCTGGCTTTGGGAGAAAGTACGGCCTGAGGCCGGGAGCAGTCGGTGGACTACCGGGCCCTGGC	
DNAPTAQC.....A.....C.....C.....CC.....A.....	557
DNAPTFLAC.....AC.....C.C.....	554
DNAPTTHA.....C.....C.....T..C.....C.T..560	
MAJORITY	GGGGGACGGCTCGGACAACCTCCCGGGGGTCAAGGGGCATCGGGGAGAAAGACCGCCGXGAAGCTGCTCXAG	
DNAPTAQ	C.....GAG.....T.....G..GAG.....T..GG..	627
DNAPTFLG..T...A.....G.....A..G....A..CGC	624
DNAPTTHT.....T.....TC.....A..	630
MAJORITY	GAGTGGGGAGCCCTGGAAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC...CXTCCGGGAGAGAAGA	
DNAPTAQGC.....C.....A.....	694
DNAPTFLT..G..C.....A.....T...T..G.....C	691
DNAPTTH	A.....A.....A.....A.AAAA.G.....	700

5/117

FIG. 2D

MAJORITY [SEQ ID NO:7]	CGGGGXCTCCTCGCCAAAGGAGCTGGCCGTTTGGCCCTGAGGGAGGGCCCTXGACCTCXTGCCCGGGGAGG	
DNAPTAQ [SEQ ID NO:1]G..T.....A.....AG.....C.....A.....T.G.....CC.....C.....	1114
DNAPTFL [SEQ ID NO:2]AA.....G.....G.....G.....G.....T.C..A.A.....	1111
DNAPTTH [SEQ ID NO:3]C.....C.....C.....TC.....G..A.....G.....	1120
MAJORITY	ACCCCATGCTCCTCGCCCTACCTCCTGGAGCCCTCGAACACACAGCCCGGAGGGGGTGGCCCGGGGCTACGG	
DNAPTAQT.....	1184
DNAPTFLG.....T.....T.....T.....T.....	1181
DNAPTTHG.....T.....T.....T.....G.....	1190
MAJORITY	GGGGGAGTGGACGGAGGAXGGGGGGGAGCGGGCCCTCCTXTCGGAGAGGCTCTTCCXGAACCTXXGCGAG	
DNAPTAQ	C.....G.....G.....GC...T.....GCC.....GCC.....GTG..G..	1254
DNAPTFLT.....A.....GG.....C.C.....A..C...AAA.....	1251
DNAPTTHC..C.GCC.C.....C..G.....CAT.G.....CCTTA..	1260
MAJORITY	CGGCTTGAGGGGGAGGAGAGGCTCCTTTGGCTTTACGAGGAGGTGGAGAGCCCCCTTCCCGGGTGGTGG	
DNAPTAQ	A.G.....A.....G.....G.....G.....GCT.....	1324
DNAPTFLA...A..A..AC.C..G.....G.....G.....GT...	1321
DNAPTTHC.....A.....C.....C.....A.....G.....	1330
MAJORITY	CCACATGGAGGGCCACGGGGGTXCGGCTGGAGGCTGGCCCTACCTCCAGGGCCCTXTCCTGGAGGTGGCGGA	
DNAPTAQG..C.....T...AG....T.G.....C..	1394
DNAPTFLGG.....C.....C.....C.....A..C	1391
DNAPTTHC.....A.....T.....T.....C.T.....	1400

FIG. 2E

MAJORITY [SEQ ID NO:7]	GGAGATCCGGCCGCTCGAGGAGGAGGTCTTCGGGCTGGCGGGGAGCCCTTCAAGCTCAAGTCCGGGGGAC	
DNAPTAQ [SEQ ID NO:1]GC.....CC.....	1464
DNAPTFL [SEQ ID NO:2]G.G....AG..G.....	1461
DNAPTTH [SEQ ID NO:3]T.....G.....	1470
MAJORITY	CAGCTGCAAGGGTGCTCTTGACGAGCTXGGGCTTCCGGCCATCGGCAAGACGGAGAGACXGGCAAGC	
DNAPTAQC.....A.....	1534
DNAPTFLGC.....G..G..G..T.....	1531
DNAPTTHTA.....T.G..G.....C.A.....	1540
MAJORITY	GCTCCACAGCGCGCGCTGCTGGAGGGGCTXCGXGAGGGCCACGCCATCGTGGAGAAGATCCTGCAGTA	
DNAPTAQC.....C..G.....	1604
DNAPTFLT.....G..A.....CGGC.....	1601
DNAPTTHG.....A..G.....C...C..	1610
MAJORITY	CGGGGAGCTCAGCAAGCTCAAGAACAGCTACATXGACCCGCTGCCXGCGCTCGTCCAGCCGAGGACGGGGC	
DNAPTAQG....G.....T.....T....G.A....A.....	1674
DNAPTFLA.....A.....C.C...G.....A...C...	1671
DNAPTTHG.G.....C..AAG.....G.....	1680
MAJORITY	CGGCTCCACAGCGCGCTTCAACGAGACGGCCACGGCCAGGGCAGGCTTAGTAGCTCCGACCCCAACCTGC	
DNAPTAQA.....T.....C..	1744
DNAPTFLG.....C.....TGG.....	1741
DNAPTTHG.....	1750

FIG. 2F

MAJORITY [SEQ ID NO:7]	AGAACATCCCCCTCCGCACCCCTGCTGGGGCAGAGGATCCGGCCGGCCCTTCGTGGCCGAGGAGGGXTGGGT	
DNAPTAQ [SEQ ID NO:1]G..T..G.....A.C.....G...C..	1814
DNAPTFL [SEQ ID NO:2]G.....T.....C.C.....A.....C.....	1817
DNAPTTH [SEQ ID NO:3]CT.....C.....G...T.....C..	1820
MAJORITY	GTGGTGGCCCTGGACTATAGCCAGATAGAGCTCGGGGTCTGGCCACCTCTCTCCGGGGACGAGAACCTG	
DNAPTAQ	A.....A.....G.....C.....	1884
DNAPTFL	.C.....T.T.....C.....T.....	1887
DNAPTTHG.....G.....A.....	1890
MAJORITY	ATCCGGGTCTTCGAGGGGAGGGACATCCACAGCCGAGCGGCGGTGGATGTTGGGGTCCCGCCCGG	
DNAPTAQC.....GG.....G...G...	1954
DNAPTFLT.....A.....TT...C..	1951
DNAPTTH	...A.....A.....A.....	1960
MAJORITY	AGGCGGTGGACCCCTGATCGCGCCGGCGCCCAAGACCATCAACTTCGGGGTCTCTACGGGATGTCCGG	
DNAPTAQG.....G...G...G...	2024
DNAPTFL	.A.GG..A...T.....G.....	2021
DNAPTTHGG.G.....C.....	2030
MAJORITY	CCACGGCCCTCTCCGAGGAGGTTGGCATCCGCTACGAGGAGGGGTGGCCCTTCATTGAGCGGTACTTCCAG	
DNAPTAQA.....T.....CCA.....T...	2094
DNAPTFLGG.....T.....	2097
DNAPTTH	...TA.G.....T..A.....A	2100

FIG. 2G

MAJORITY [SEQ ID NO:7]	AGCTTCCGCAAGGTGGGGGGCTGGATTGAGAAAGACCCCTGGAGGAGGGGACGAGGGGGGTACGTGGAGA	
DNAPTAA [SEQ ID NO:1]	2164
DNAPTFL [SEQ ID NO:2]	...A.....GG.....C.....C.CC.....T.....	2161
DNAPTTH [SEQ ID NO:3]A.A.....G.....A.....C.....A.	2170
MAJORITY	CCCTCTTCCGGCCGGCGGCTACGTGCCCGACCTCAACGCCCGGCTGAAGAGCGTCCGGGAGCGCGCGGA	
DNAPTAAC.....A.....AG.G.....C...	2234
DNAPTFLT.....C.....C.....	2231
DNAPTTHAA.AA.....CA.....C.....	2240
MAJORITY	GGGATGGCCTTCAACATGCCCGTCCAGGGCACCGCCCGGACCTCATGAAGCTGGCCATGGTGAAGCTC	
DNAPTAAT.....	2304
DNAPTFLG.....GG...T	2301
DNAPTTHC.....	2310
MAJORITY	TTCCCGCGGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCACGAGCGAGCTGGTCCGCGGCGCC	
DNAPTAAA...GG.....T.....	2374
DNAPTFLT...C.....G...TT.G...G.....	2371
DNAPTTHC.C.G...G.....C.C.....CG...G.....	2380
MAJORITY	CGAAAGAGCGGGCGGAGGXGGTGGCGGCTTGGCCCAAGGAGGTGATCGAGGGGGTCTATCCCGTGGCGGT	
DNAPTAAA.....CC.....GGC.....G.....	2444
DNAPTFLG.C.....AG...A.....GG.....GAG..	2441
DNAPTTHC...C.....C...A.....G.....AA..C.....C.....	2450

FIG. 2H

MAJORITY [SEQ ID NO:7]	GGCCCTGGAGGCTGGAGGCTGGGGATGGGGAGGACTGGCTCTGGGCCAAGGAGTAG
DNAPTAA [SEQ ID NO:1]A.....GA
DNAPTFL [SEQ ID NO:2]CC.....
DNAPTTH [SEQ ID NO:3]T.....GT...

FIG. 3A

MAJORITY [SEQ ID NO:8]	MXAML PLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPUQAVYGFAKSLIKALKEDG-DAXVVVFDAK	
TAQ PRO [SEQ ID NO:4]	RG.....H.....	69
TFL PRO [SEQ ID NO:5]V.V.....	68
TTH PRO [SEQ ID NO:6]	E.....YK..F.....	70
MAJORITY	APSRHEAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEVPGEYADDVLATLAKKAEKEGYEVRL	
TAQ PRO	GG.....A.....S.....	139
TFL PROV.....F.....R.....	138
TTH PROFT.....	140
MAJORITY	TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPDSNLPGVKGI GEKTAXKLLX	
TAQ PRO	K.....H.....D..A...T..E.....R...E	209
TFL PROE...I.....Y.....A.....I.....QR..I	208
TTH PRO	V...V.....H...E.....F...V.....L...K	210
MAJORITY	EWGSLNLLKNLDRVKP-XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDRGLRAFLEF	
TAQ PRO	A.....L...AI...L...D...K..WD.AK.....K.....R.....	278
TFL PRO	FOH..Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTH PRO	ENV.....K..L...R..LE..R.....L.OG.....	280
MAJORITY	GSLHFEGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAE LLALAAARXGRVHRAXDPLXGLRDLKEV	
TAQ PRO	S.....K.....D.....G.....PE.YKA.....A	348
TFL PRO	G...A.....L..SF.....G.WE..L...Q...R.....G.	347
TTH PRO	A.AP.....K.....G.D.....A...A..K.....	350

FIG. 3B

MAJORITY [SEQ ID NO:8]	RGLLAKDLAVLALREGLDXPODDPMLLAYLLDPSNTTPEGVARRYGGEWTEADAGERALLSERLFXNLXX	
TAQ PRO [SEQ ID NO:4]S.....G.P.....E.....A.....A.....WG	418
TFL PRO [SEQ ID NO:5]I.....F.E.....A.....QT.KE	417
TTH PRO [SEQ ID NO:6]S.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRLEEEVFRLAGHPFNLNSRD	
TAQ PROR...R...A.....R.....A.....	488
TFL PROK.....E.....R.....EA.V.Q.....	487
TTH PROK.....H.....L.....	490
MAJORITY	QLERVLFDELGLPAIGKTEKTKRSTSAAVLEALREAHPIVEKILOYRELTCLKNTYIDPLPXLVHPRTG	
TAQ PROS.....D.I.....	558
TFL PRODR.....A.....K..	557
TTH PROR...L...Q.....H.....V.....S.....	560
MAJORITY	RLHTRFNOTATATGRSSSDPNLQNI PVRTPLGQRI RRAFVAEEGWXLVALDYSOIELRVLAHLSGDENI	
TAQ PROI.....L.....	628
TFL PROV...V.....	627
TTH PROA...A.....	630
MAJORITY	IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHLRSOELAI PYEEAVAFIERYFO	
TAQ PROE.....R.....Q.....	698
TFL PROS..G.....G..S.....	697
TTH PROK.....V.....	700

FIG. 3C

MAJORITY	[SEQ ID NO:8]	SFPKVRAWI EKTLEECRRRGYVETLFGRRRYVPDLNARVKSUREAAERMAFNMPVOGTAADLMKLAHVKL	
TAQ PRO	[SEQ ID NO:4]E.....	768
TFL PRO	[SEQ ID NO:5]	.Y.....G.....	767
TTM PRO	[SEQ ID NO:6]K.....	770
MAJORITY FPRLXEMGARM LQVHDELVL EAPKXRAEXVAALAKEVME GUYPLAVPLEVEVGXGEDWLSAKEX			
TAQ PROE.....E.....A.....R.....	833
TFL PROQ.L.....D.....R.....W..Q.....L.....	831
TTM PROR.....L.....QA.....E.....A..KA.....M.....G		835

Genes for Wild-Type and Pol(-)DNAPTaq

Domain

Coding Regions: 5' Nuclease

Polymerase

FIG. 4A

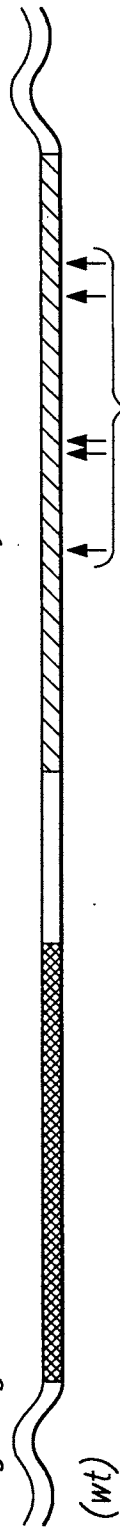


FIG. 4B

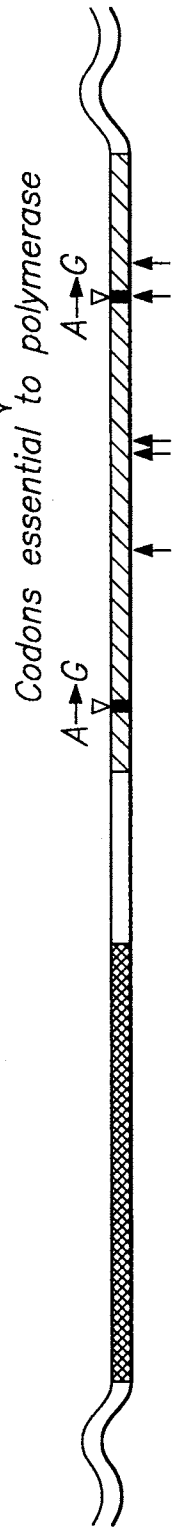


FIG. 4C



FIG. 4D

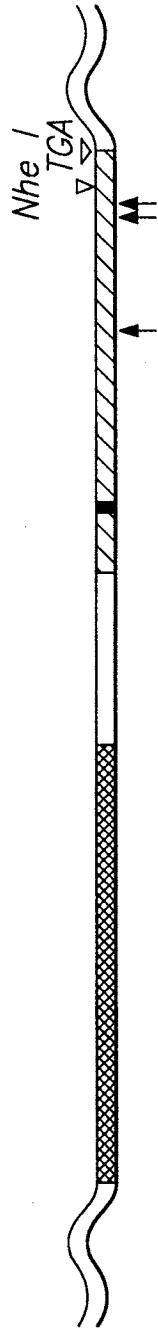


FIG. 4E



FIG. 4F

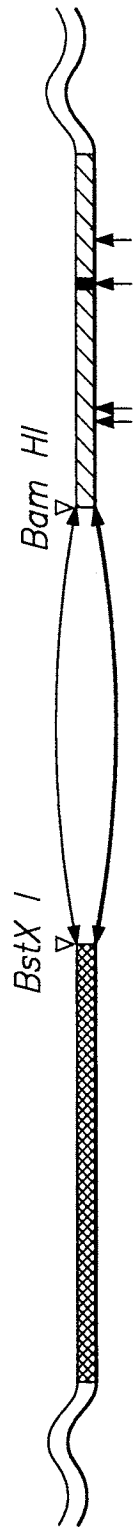
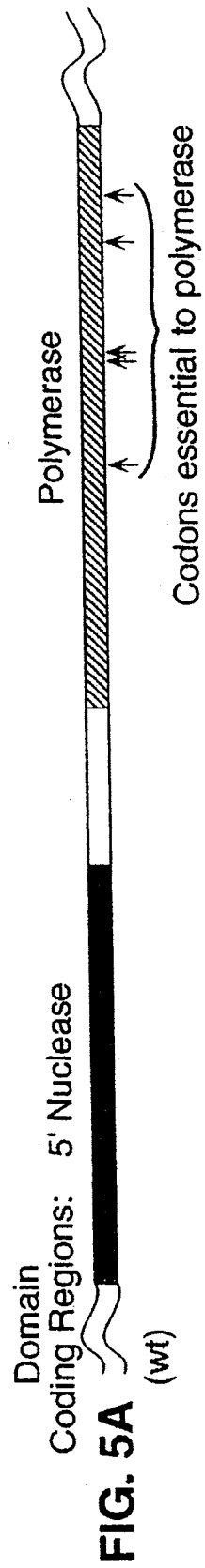


FIG. 4G



Genes for Wild-Type and Pol(-) DNAPTfl



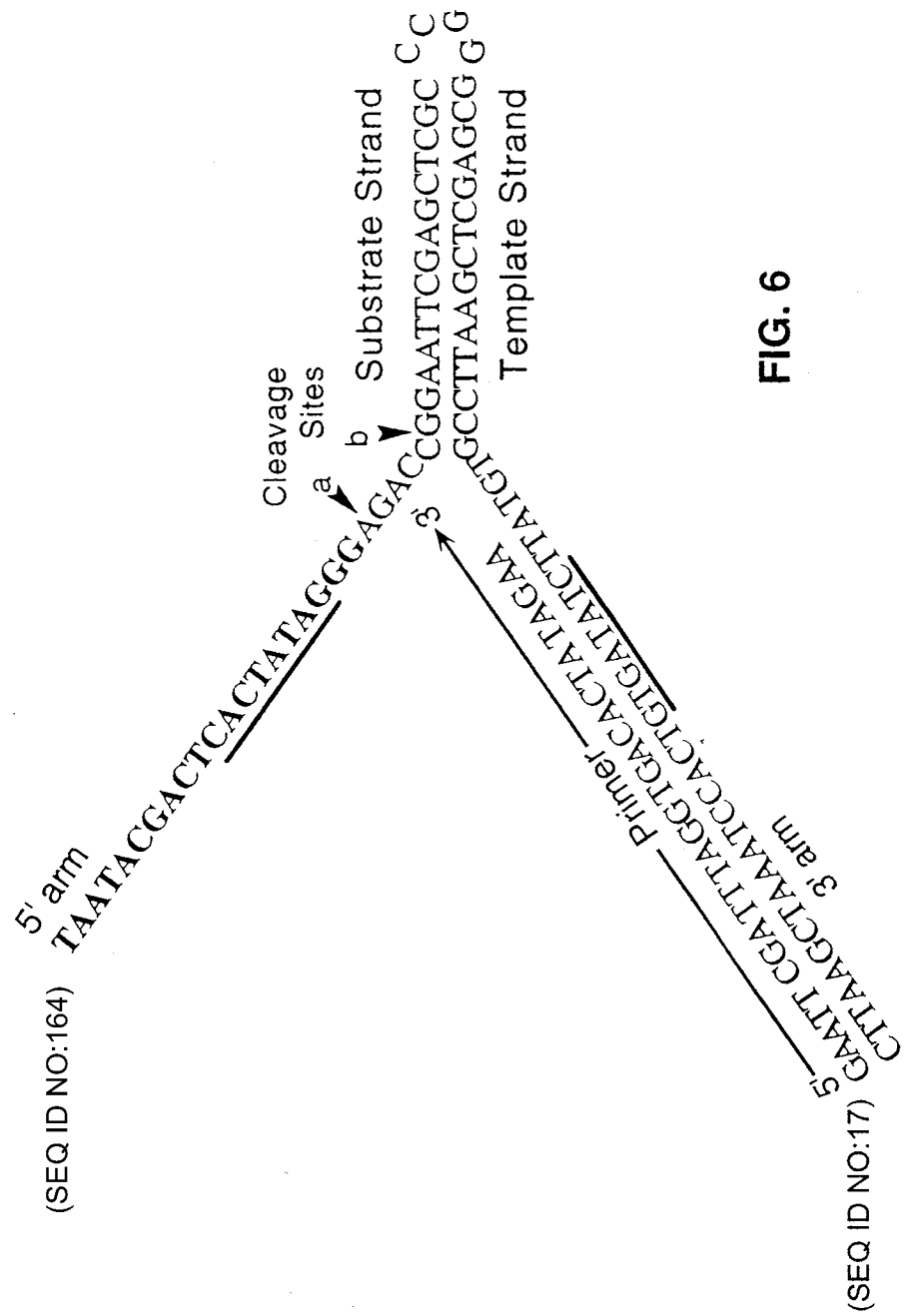
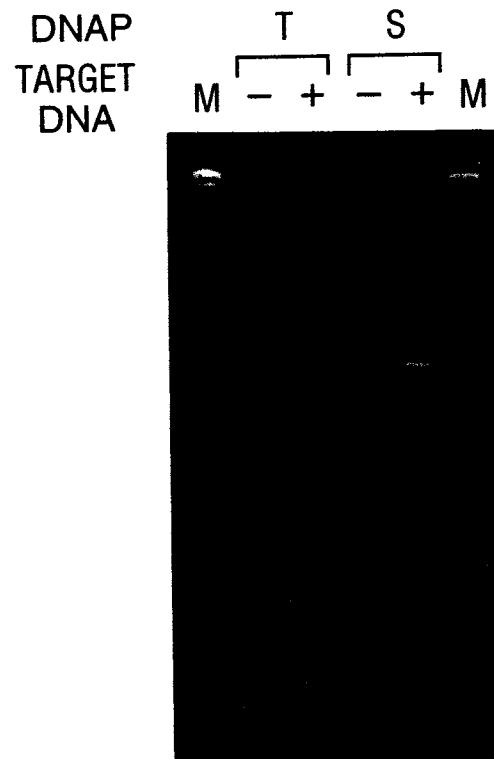
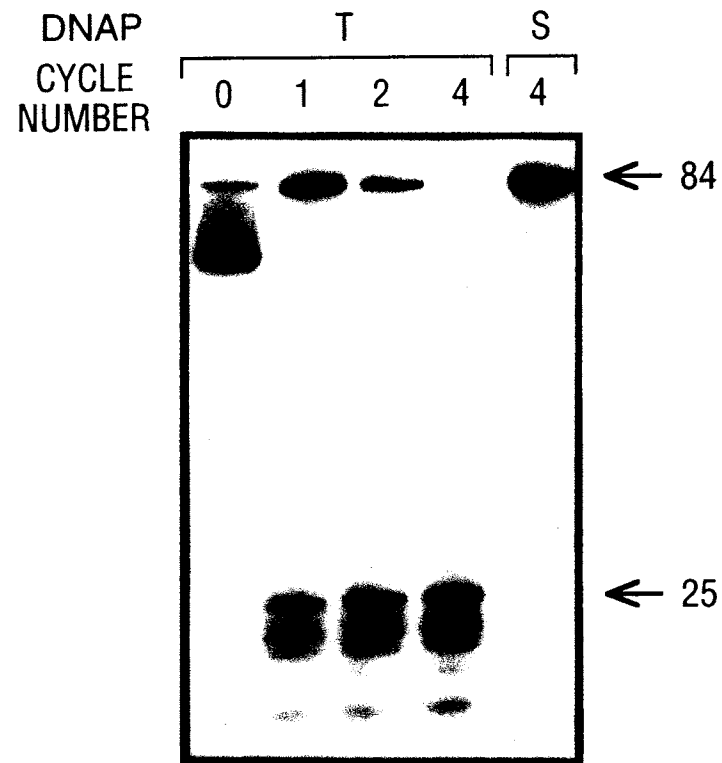


FIG. 6

**FIG. 7**

**FIG. 8**

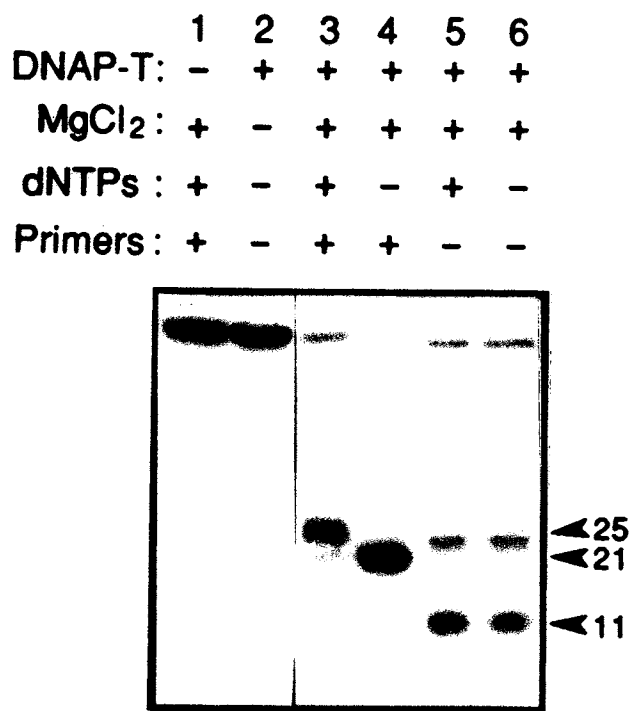


FIG. 9A

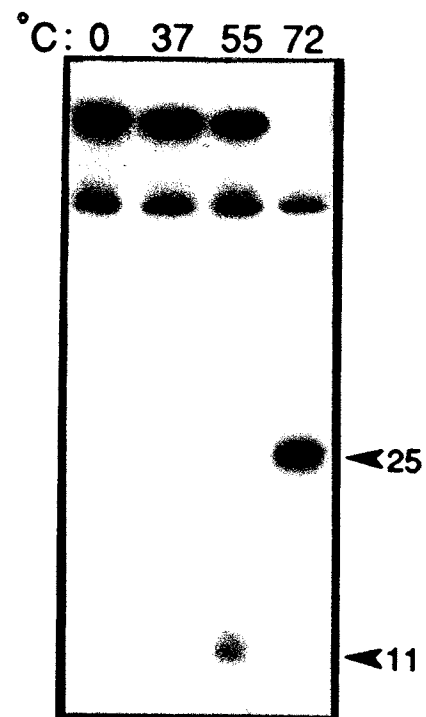


FIG. 9B

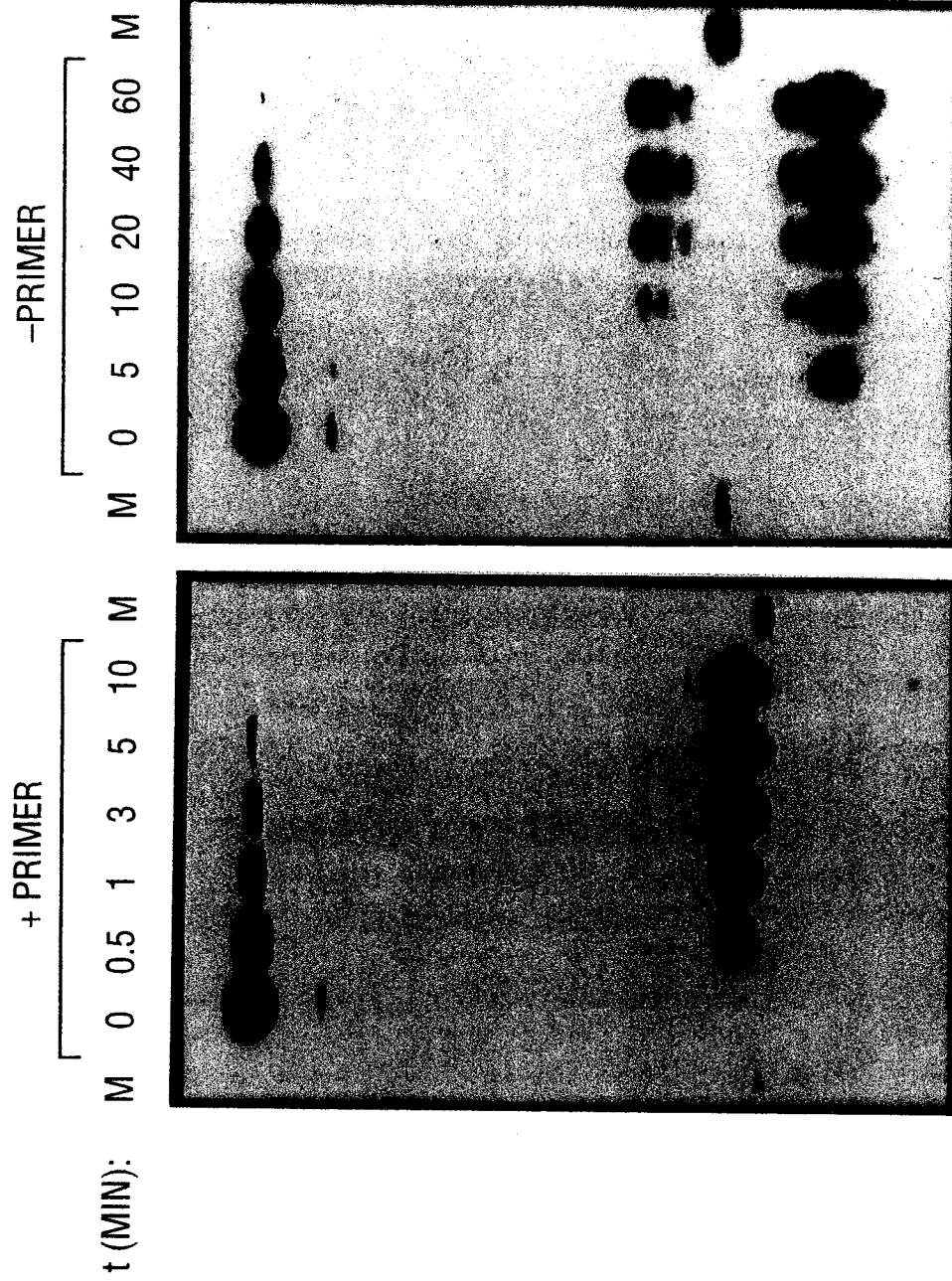


FIG. 10B

FIG. 10A

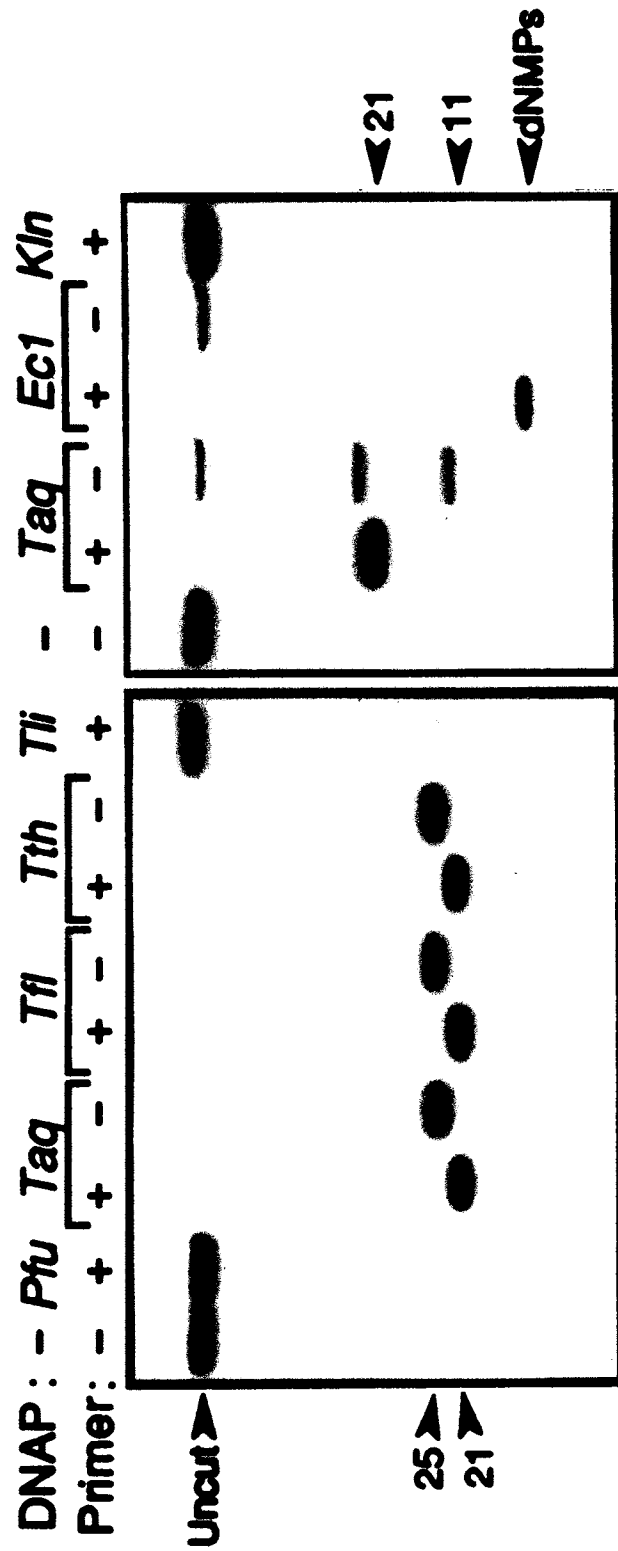
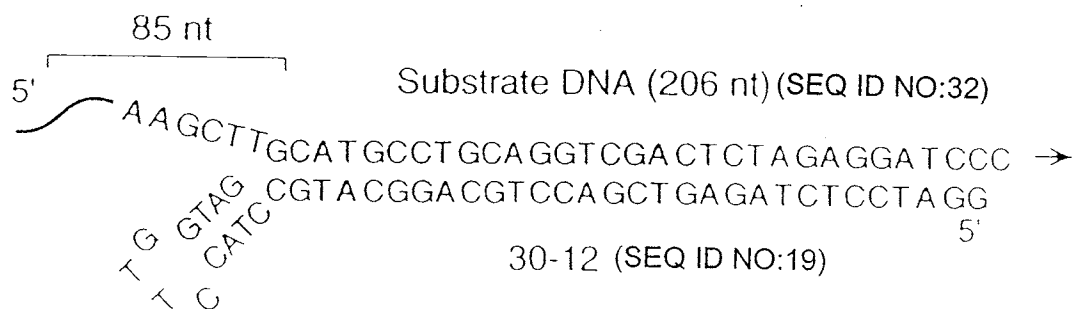
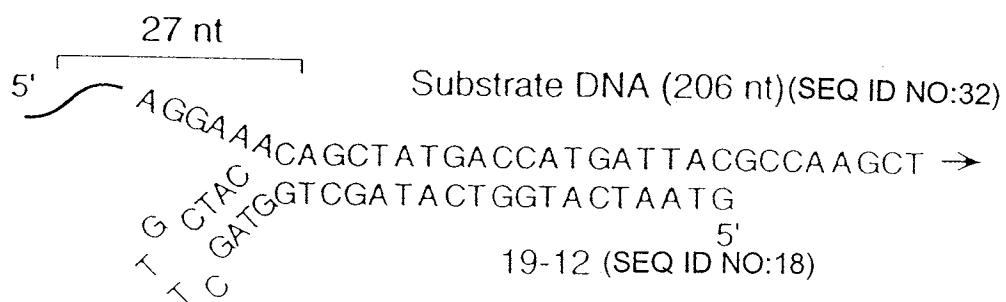


FIG. 11B

FIG. 11A

FIG. 12A



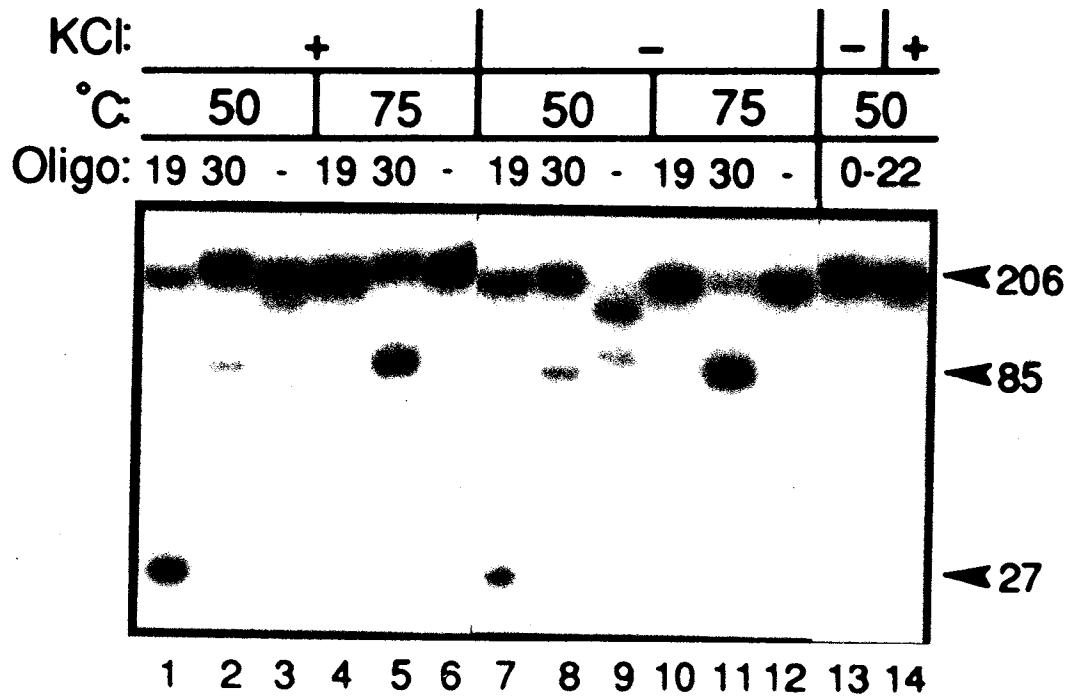


FIG. 12B

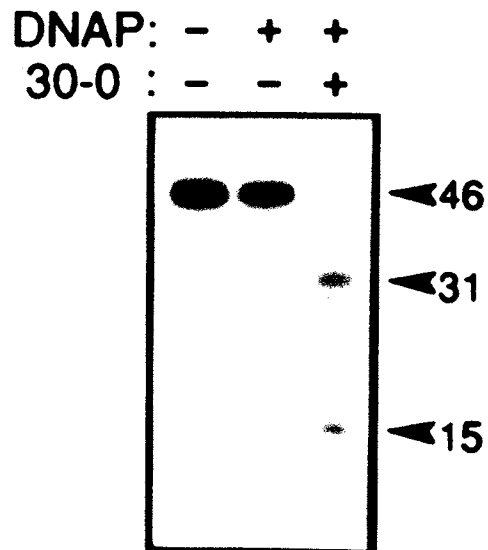


FIG. 13B

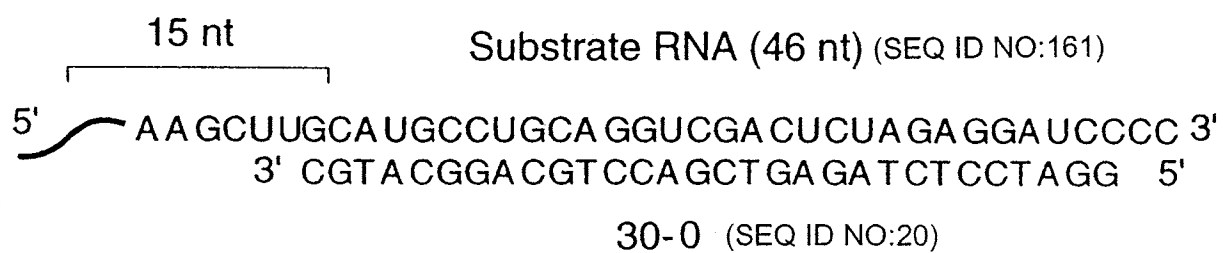
**FIG. 13A**

FIG. 14B

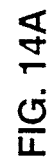
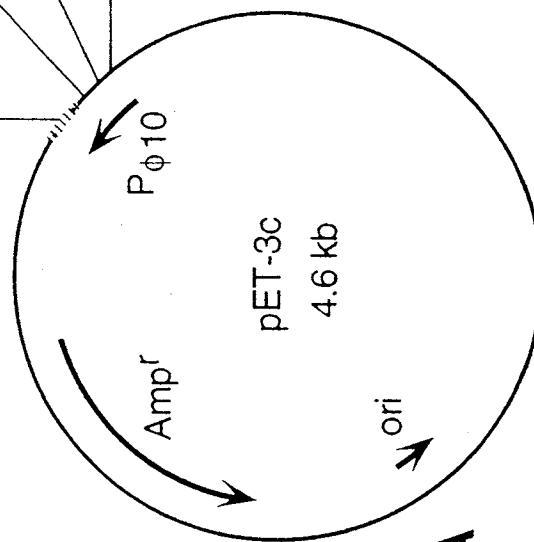
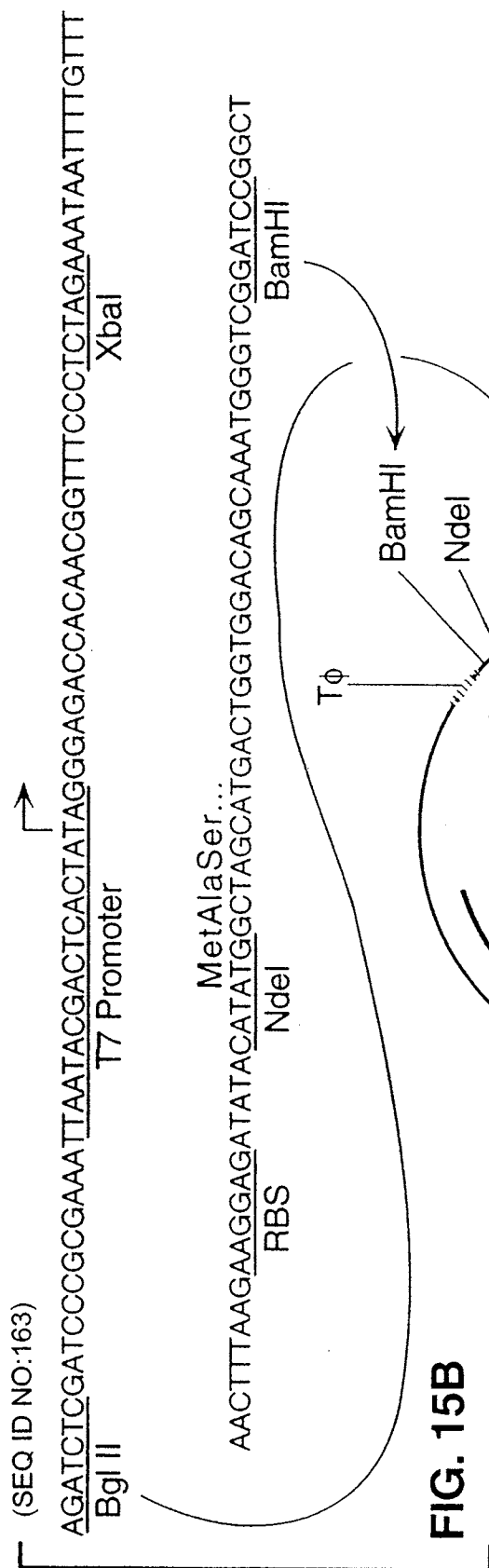


FIG. 14C



P_{φ10}: Bacteriophage T7 φ10 promoter RBS: Ribosome binding site

T_φ: T7 φ Terminator

FIG. 15C

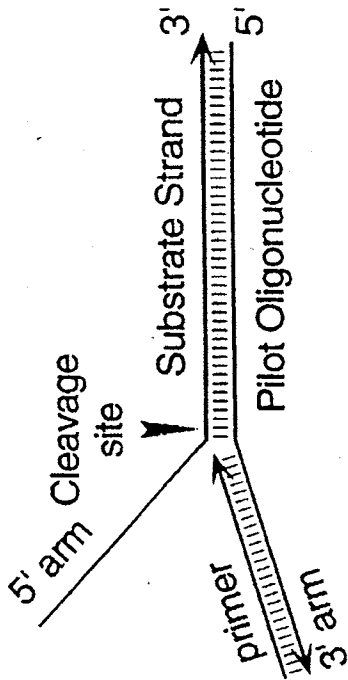


FIG. 16B

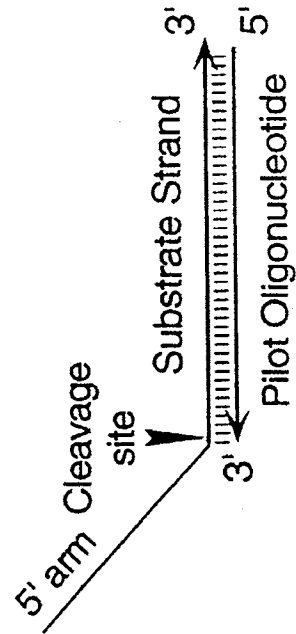


FIG. 16D

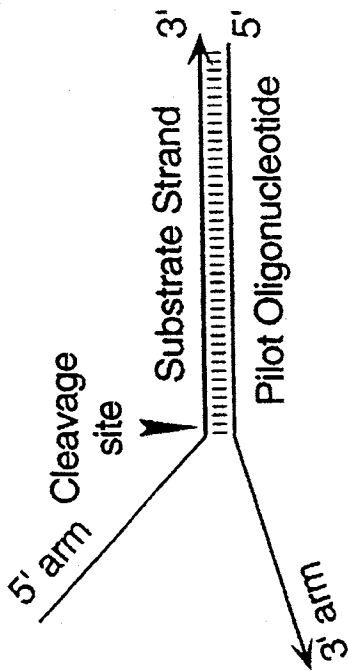


FIG. 16A

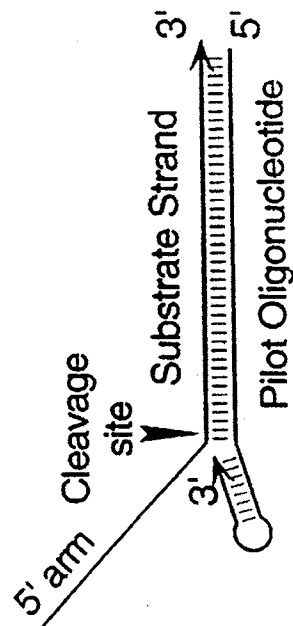


FIG. 16C

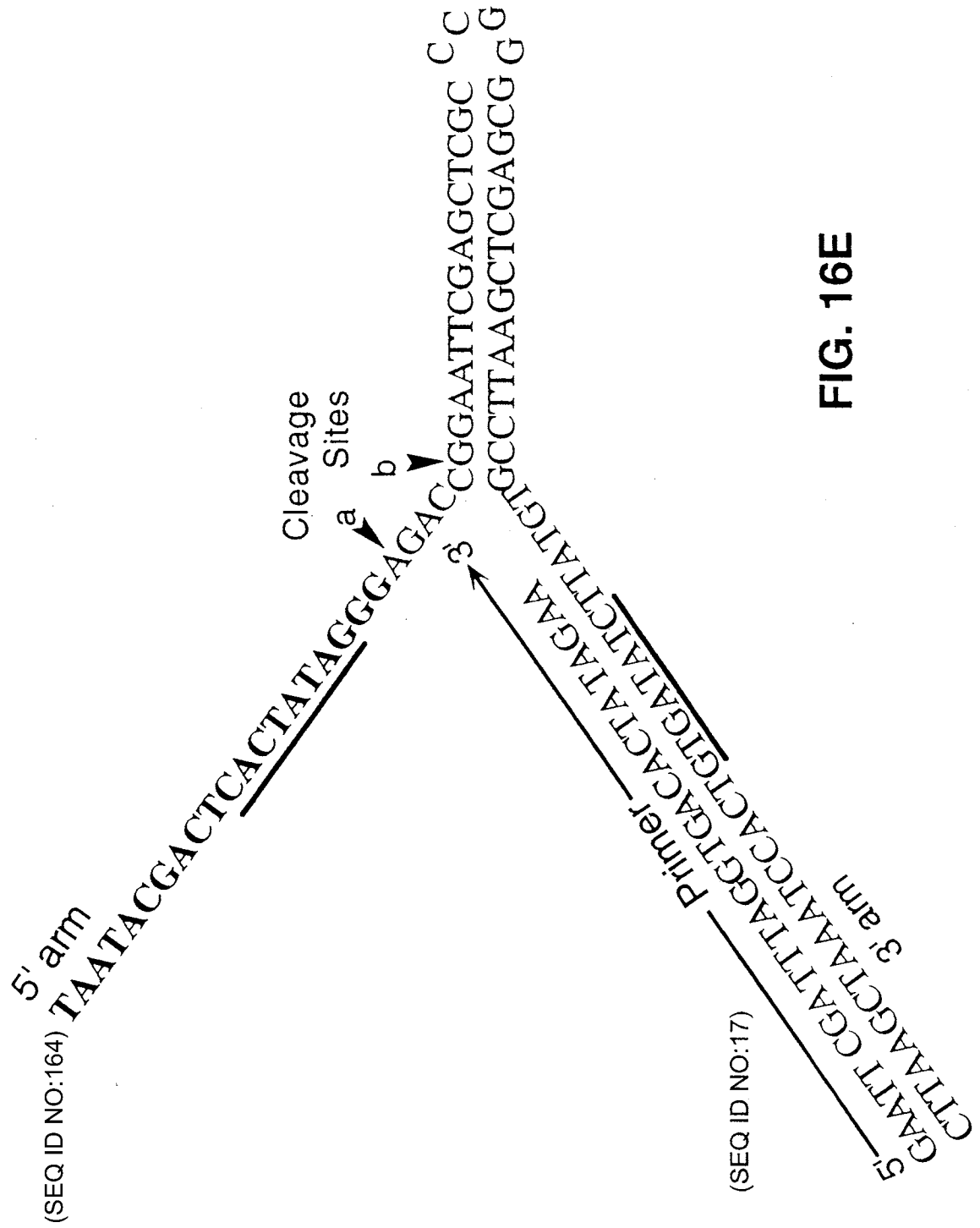


FIG. 16E

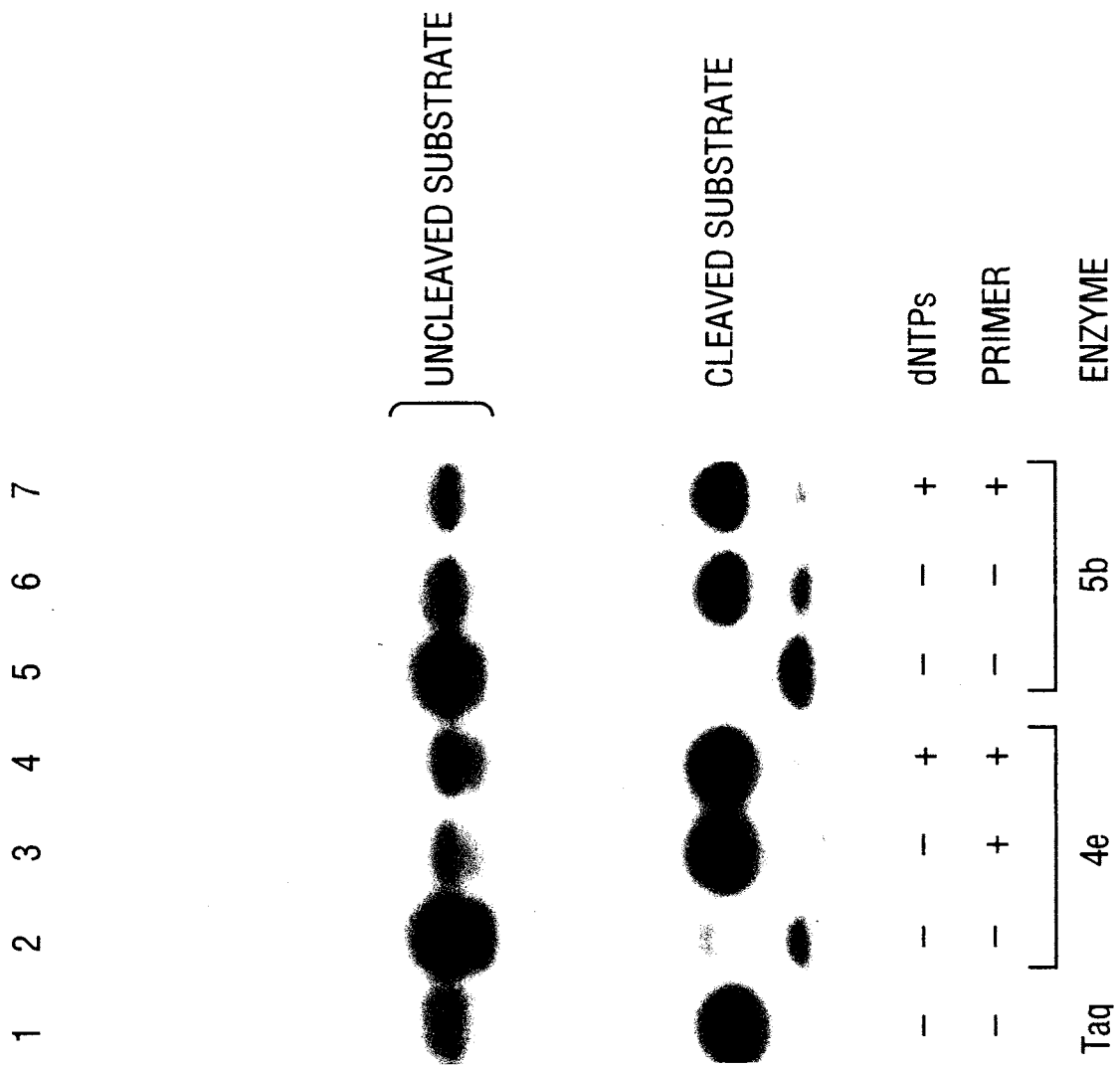


FIG. 17

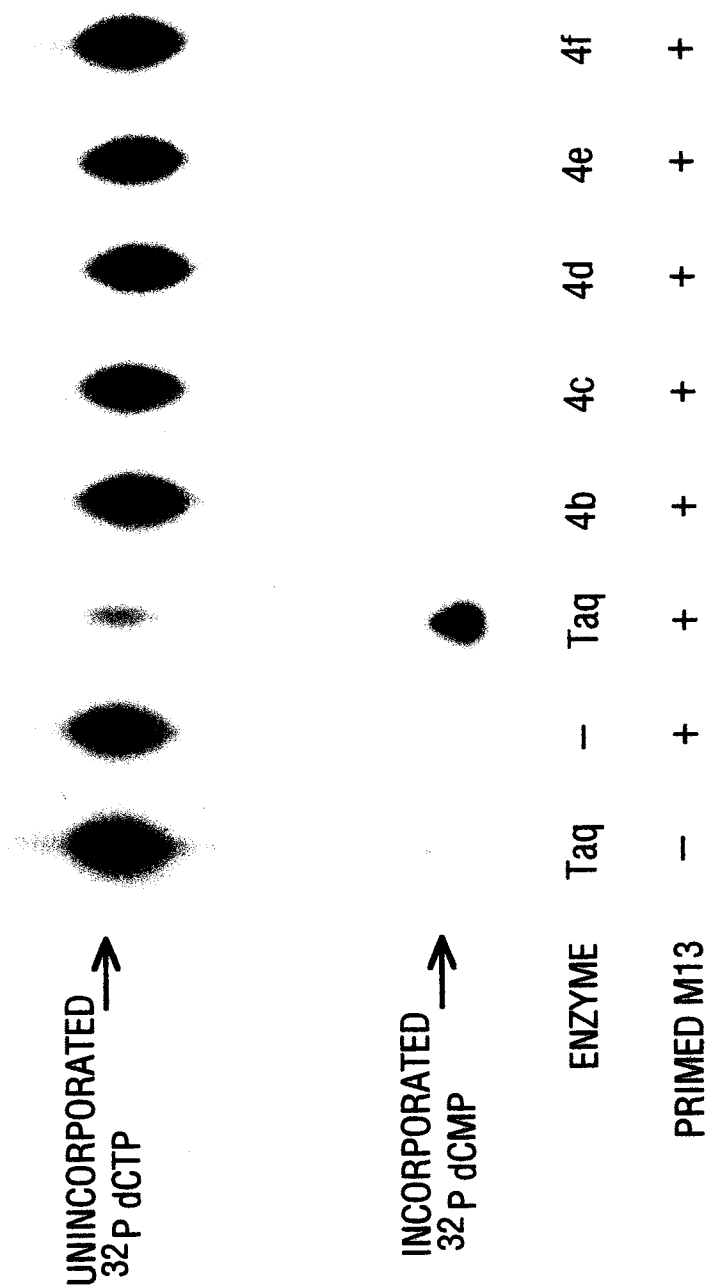
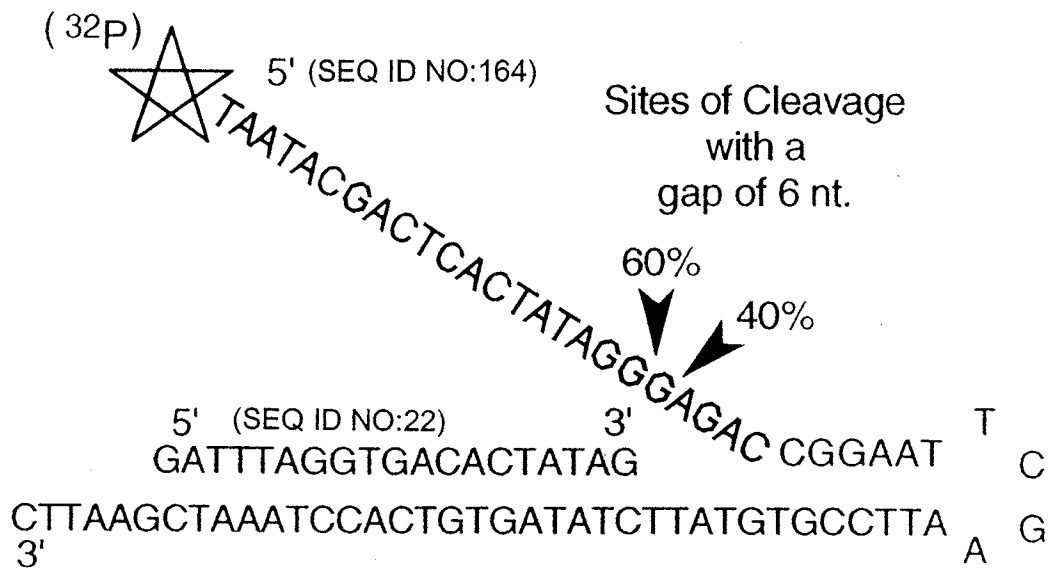
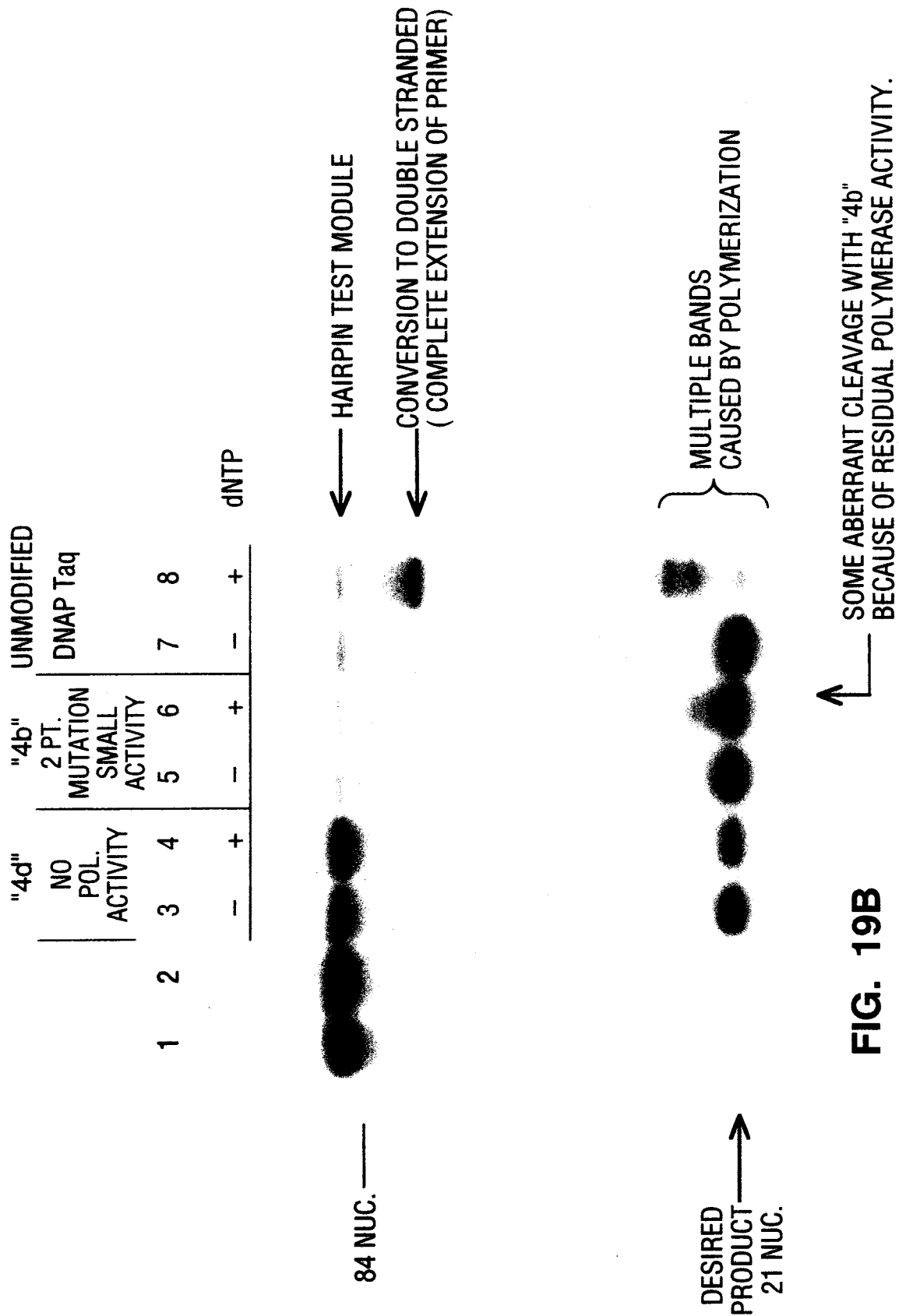


FIG. 18

**FIG. 19A**



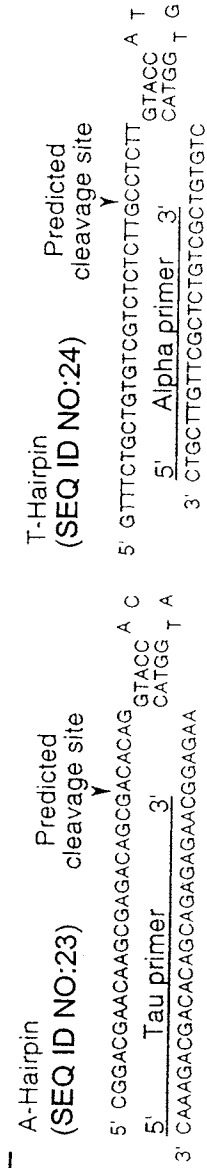


FIG. 20A

Sequence of alpha primer: (SEQ ID NO:25)

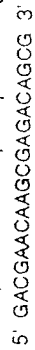


FIG. 20B

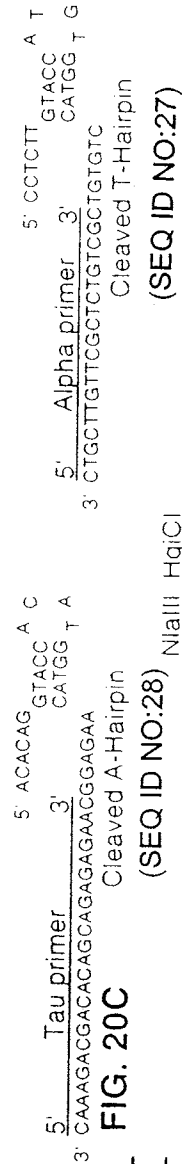


FIG. 20C

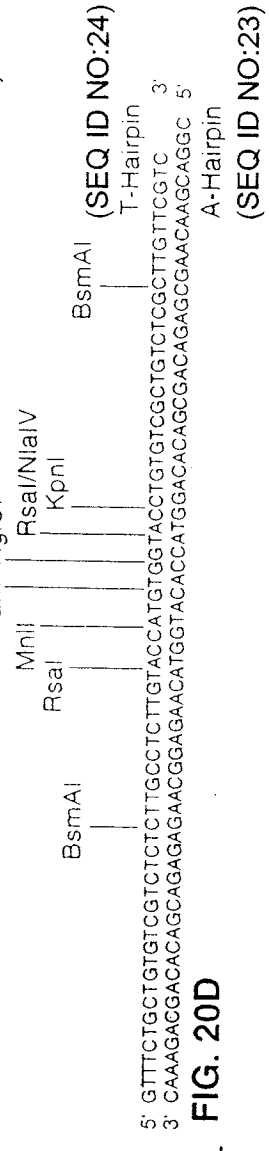
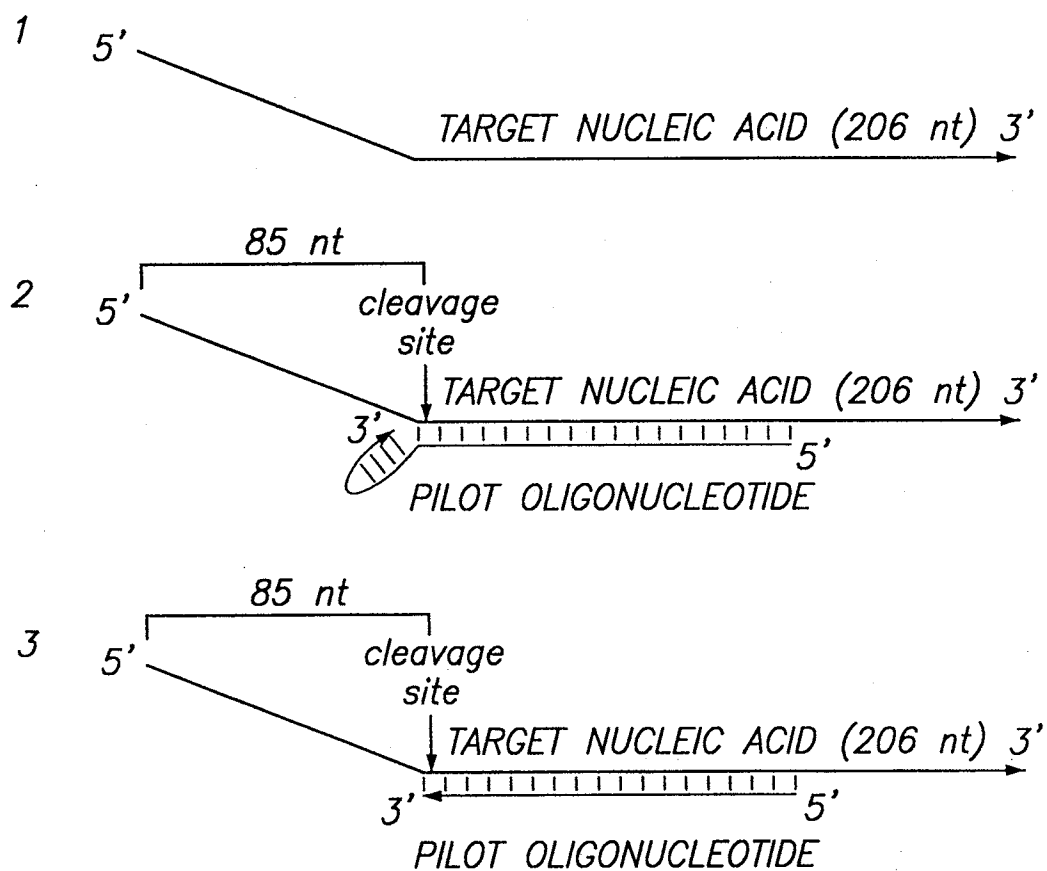


FIG. 20D

TCCGCTCAACAATTCCACACACAACATACGA
 AGCGAGTGTTTAAGGTGTGTGTATGCT
 ---48 Reverse
 206
 228

FIG. 21

**FIG. 22A**

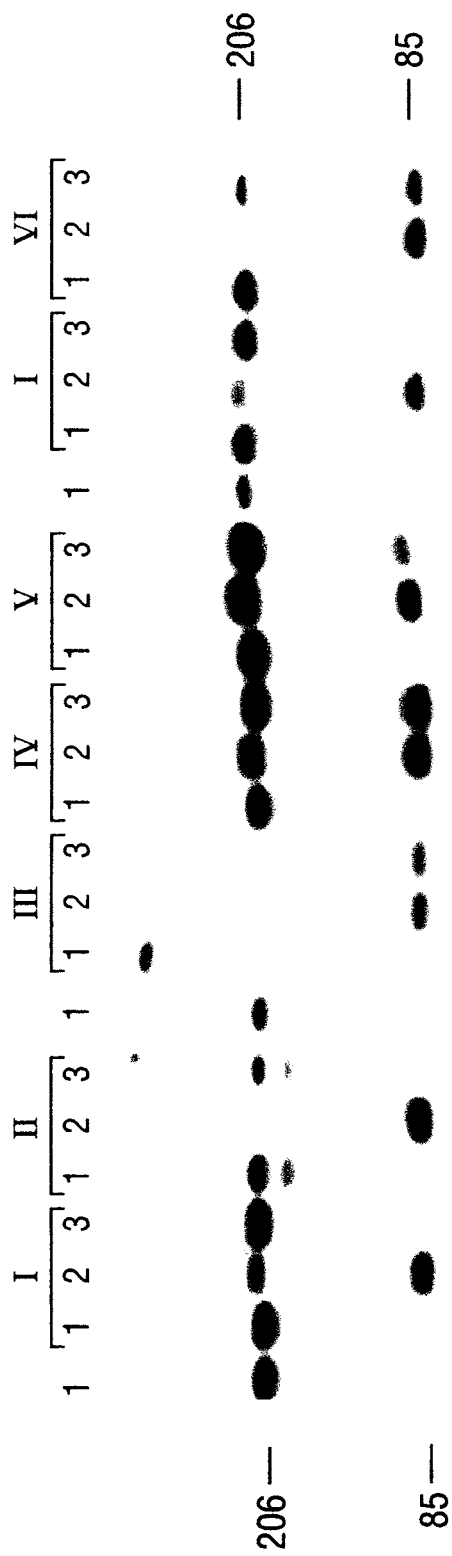


FIG. 22B

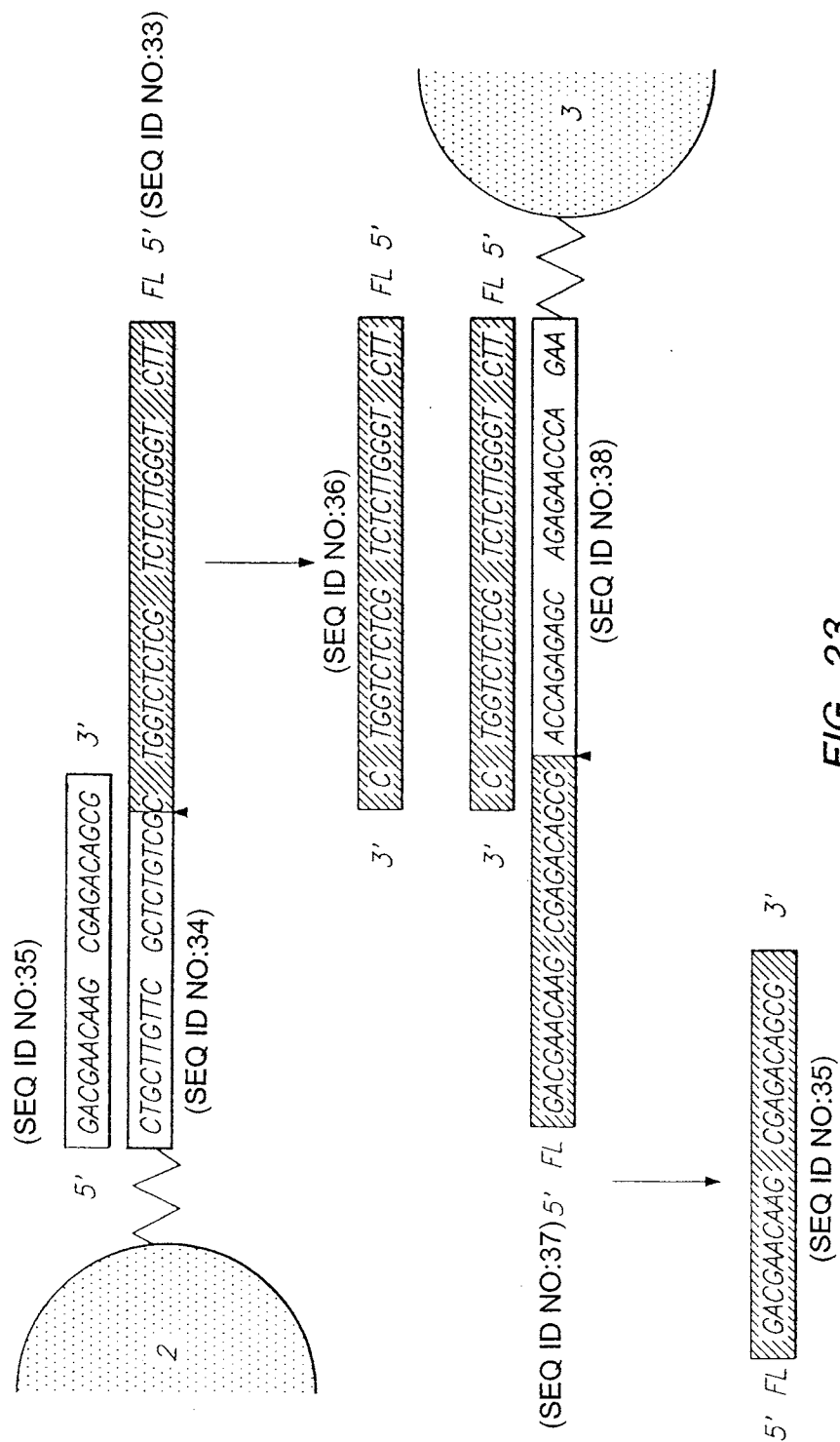


FIG. 23

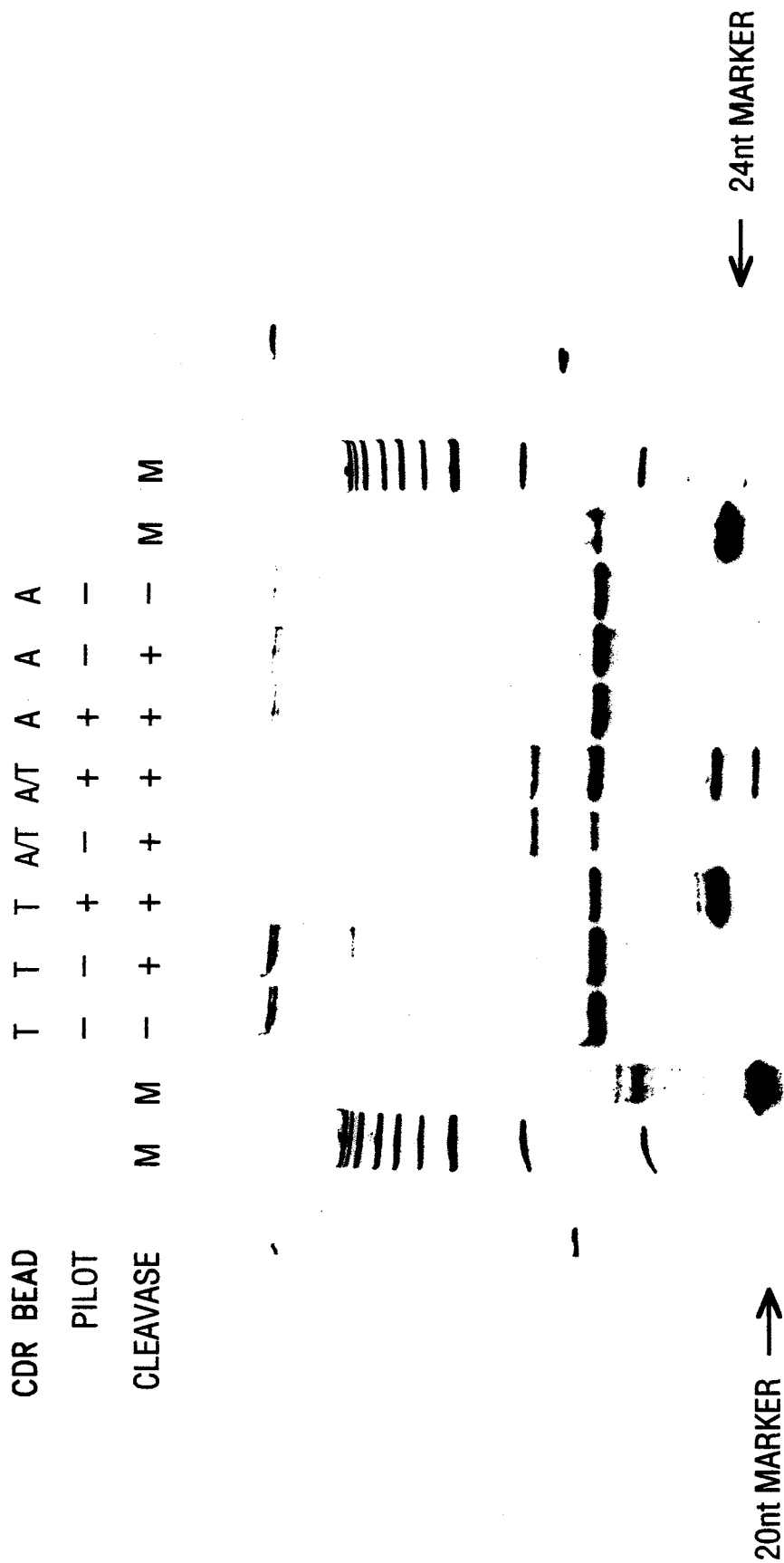


FIG. 24

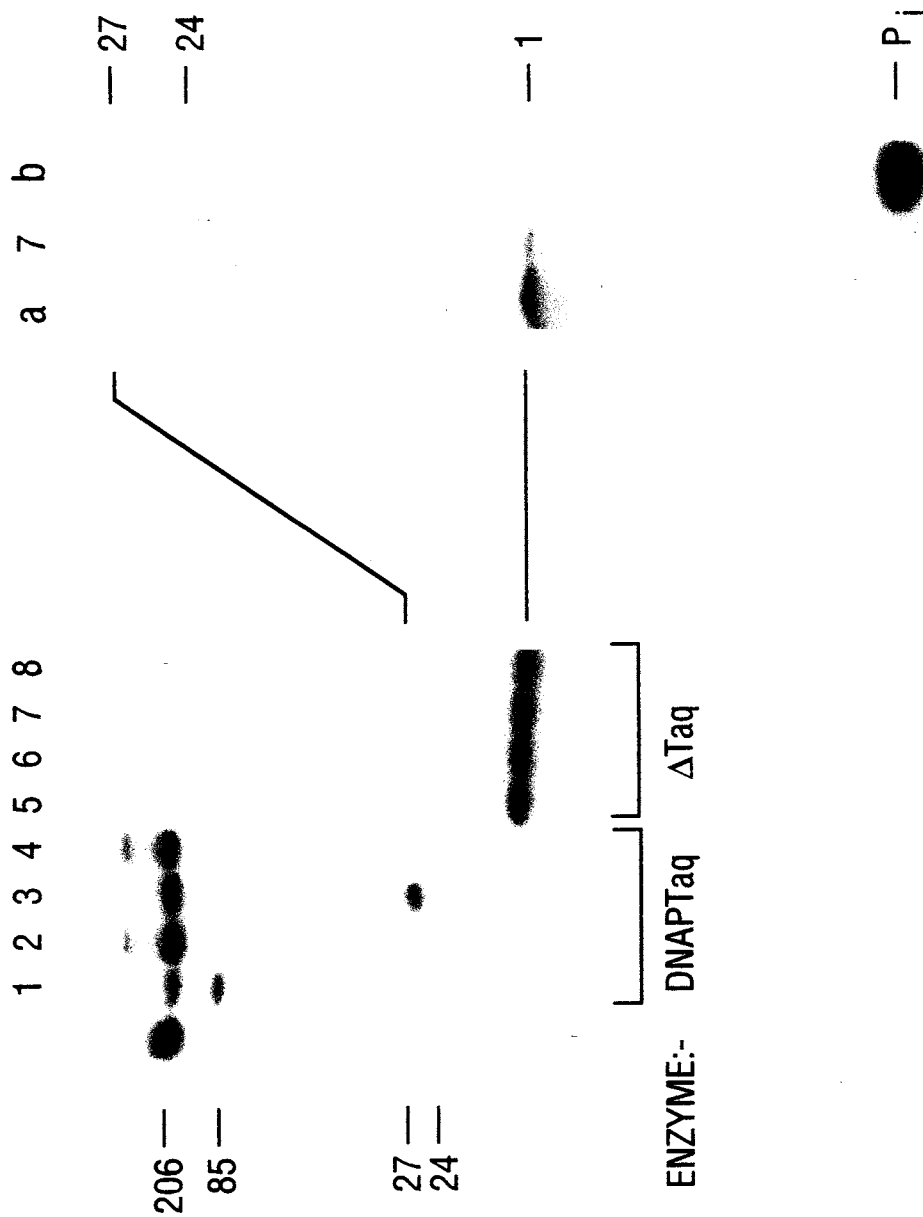


FIG. 25B

FIG. 25A

FIG. 26A

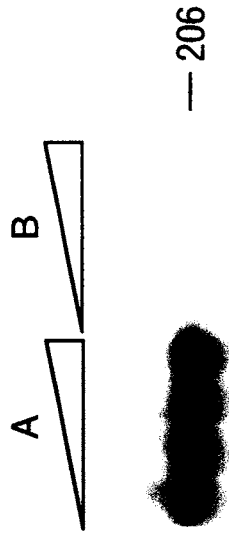
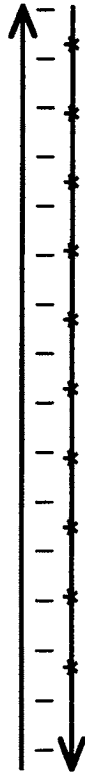
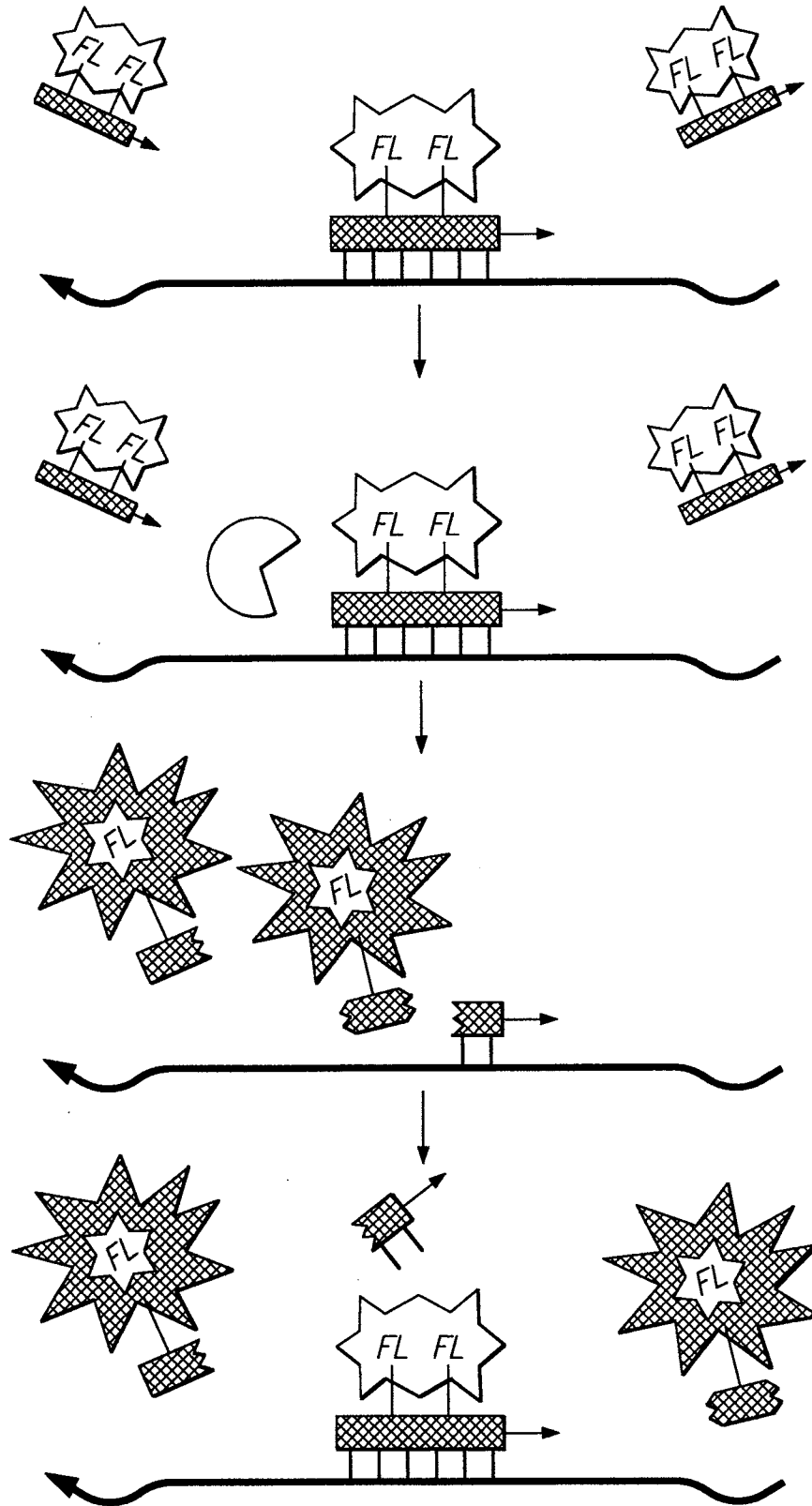
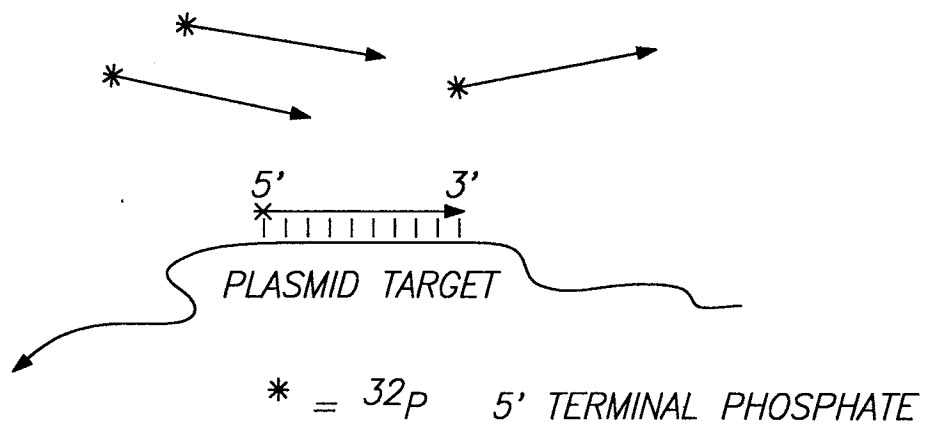


FIG. 26B



* = 32p

**FIG. 27**

**FIG. 28A**

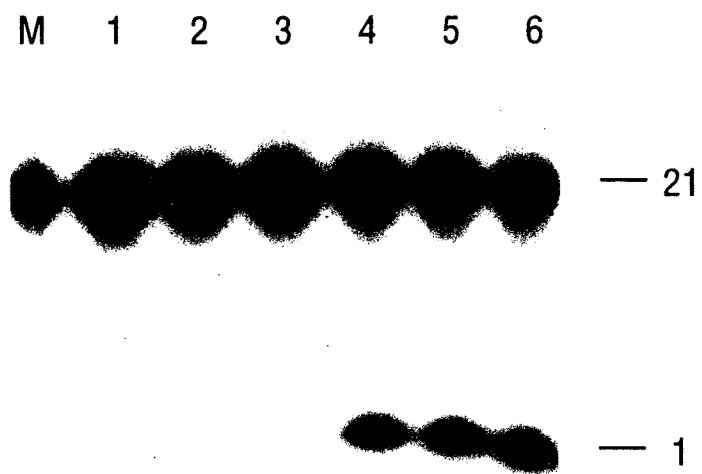
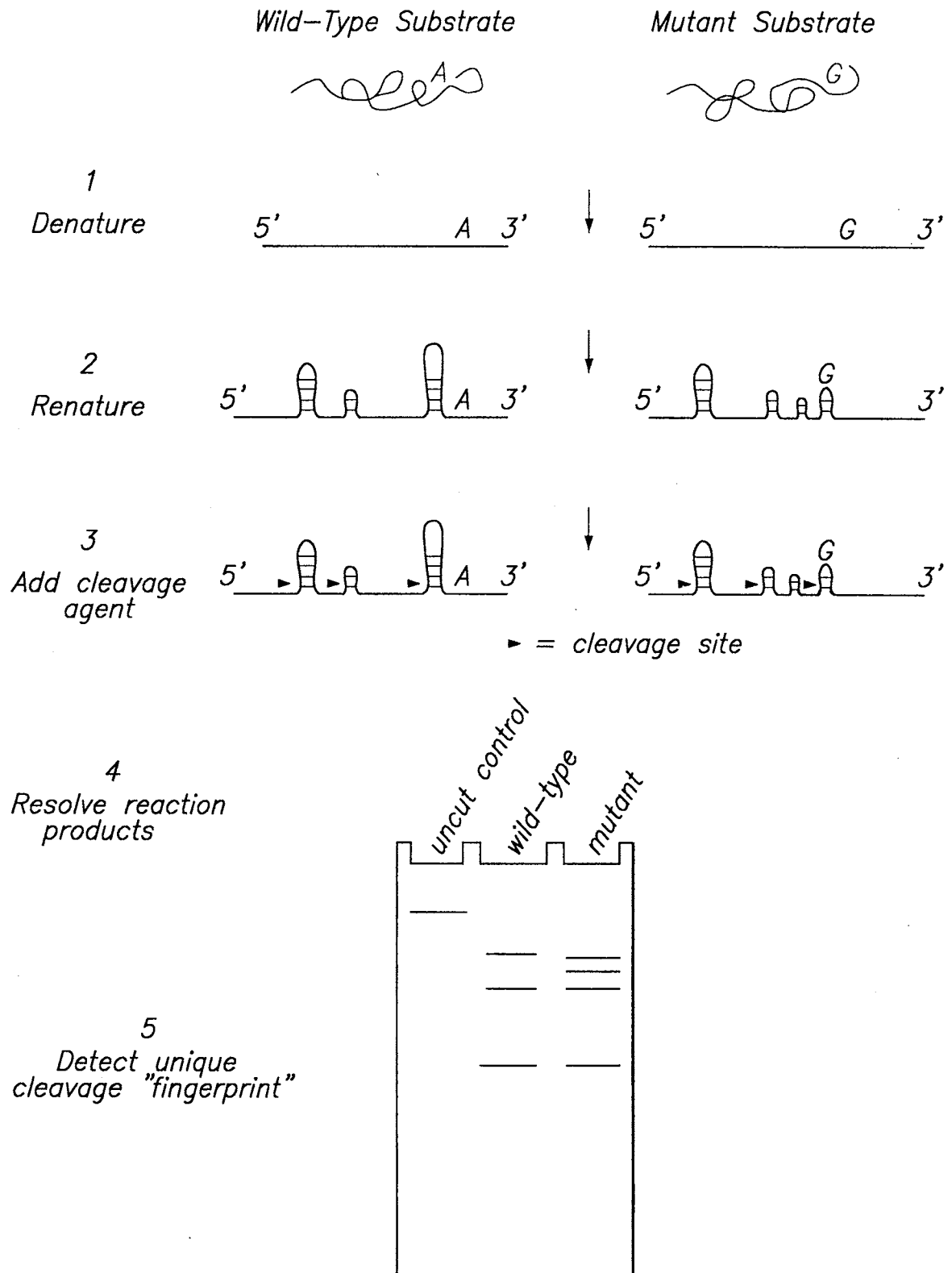


FIG. 28B

**FIG. 29**

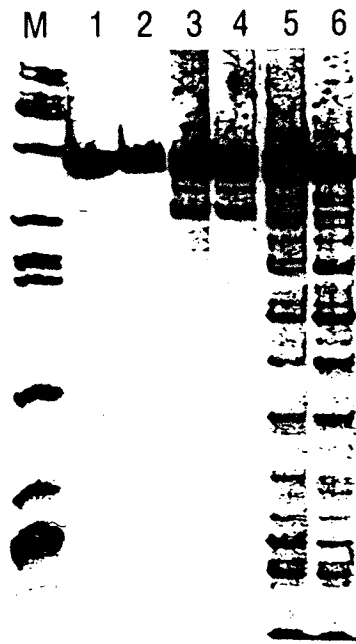


FIG. 30

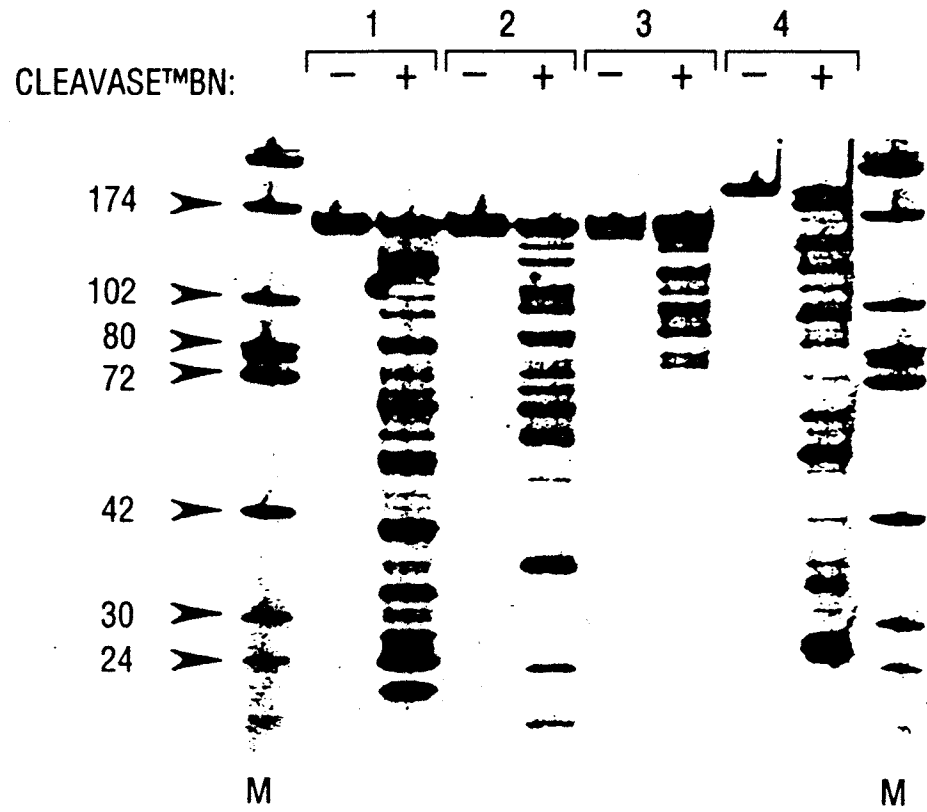
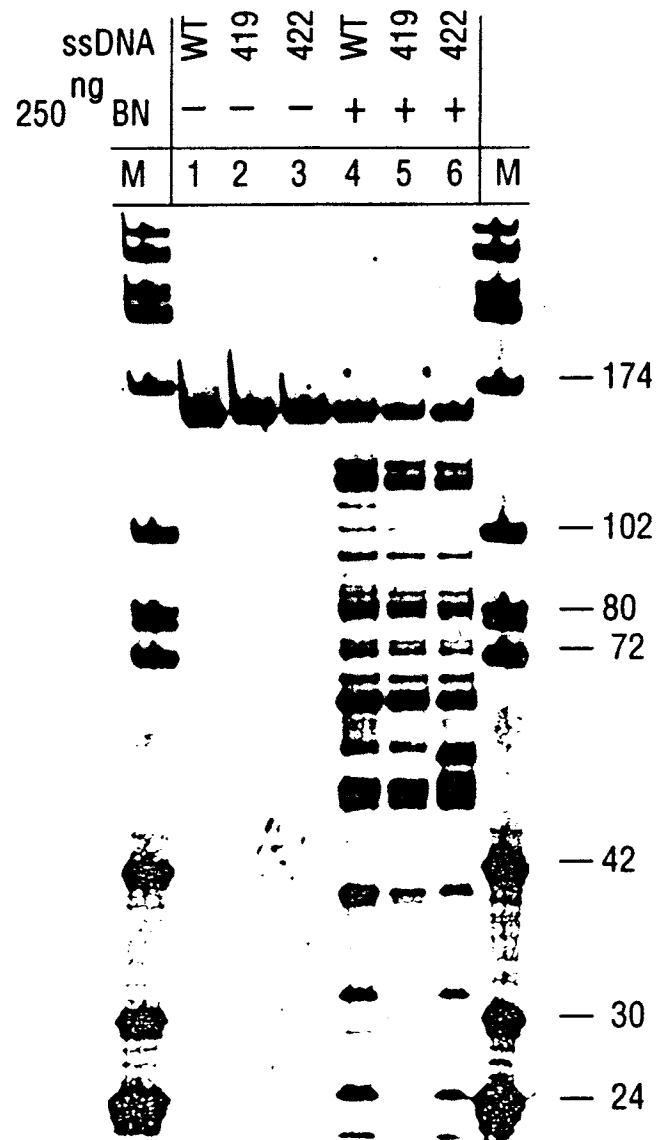


FIG. 31

**FIG. 32**

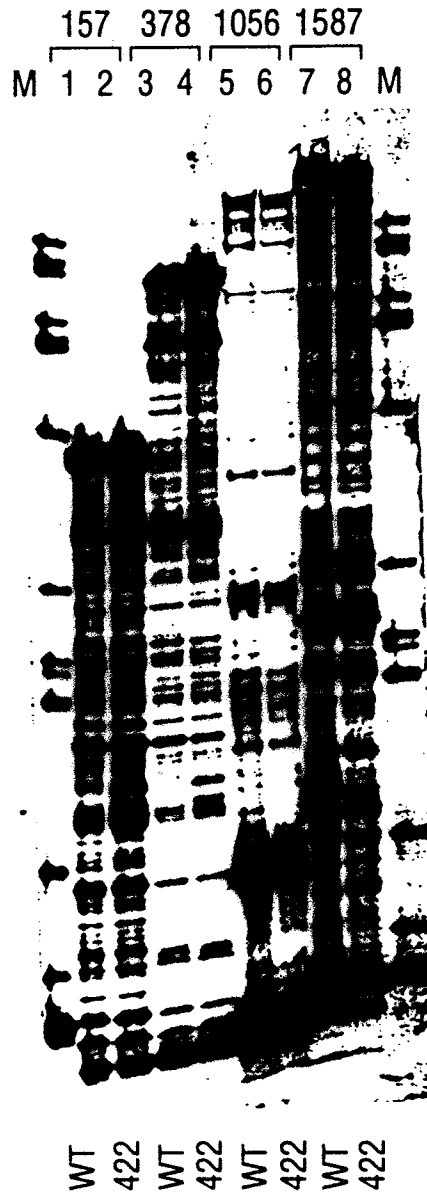
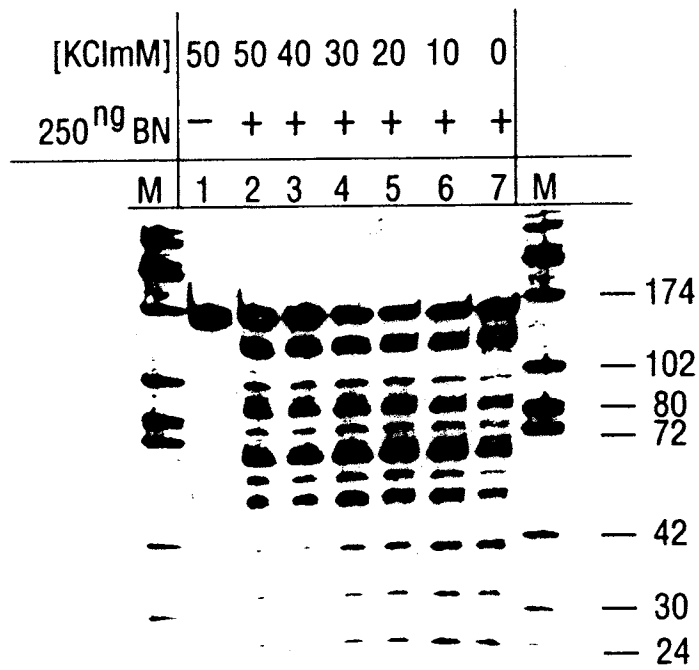
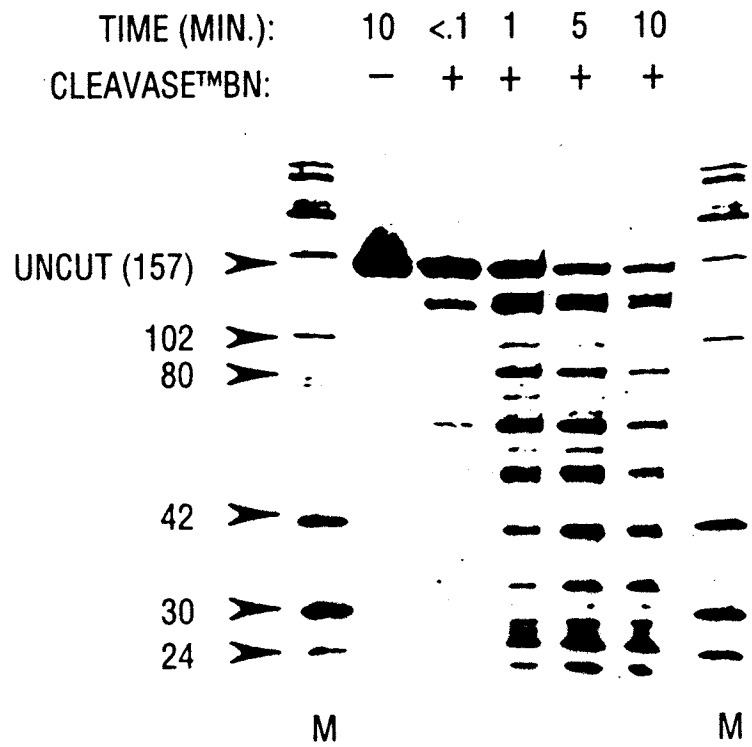
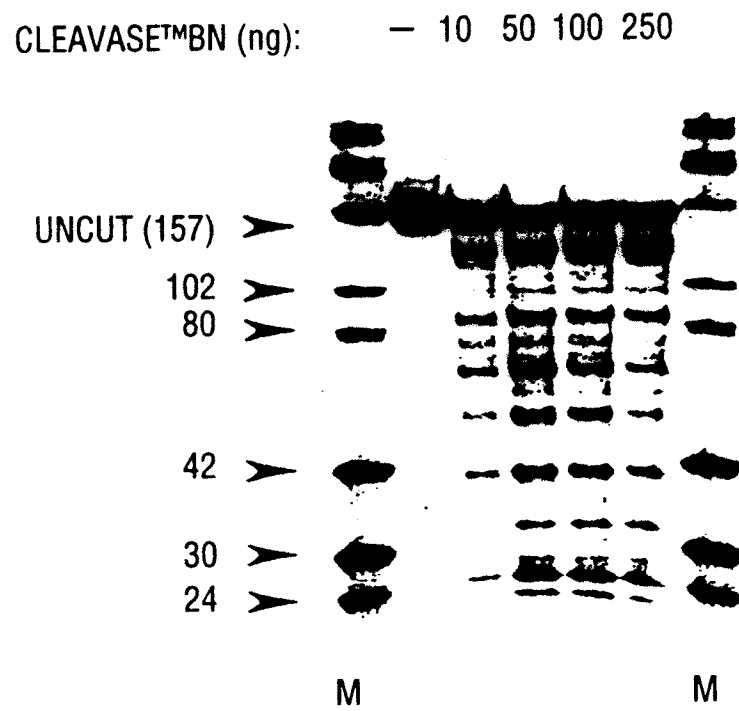
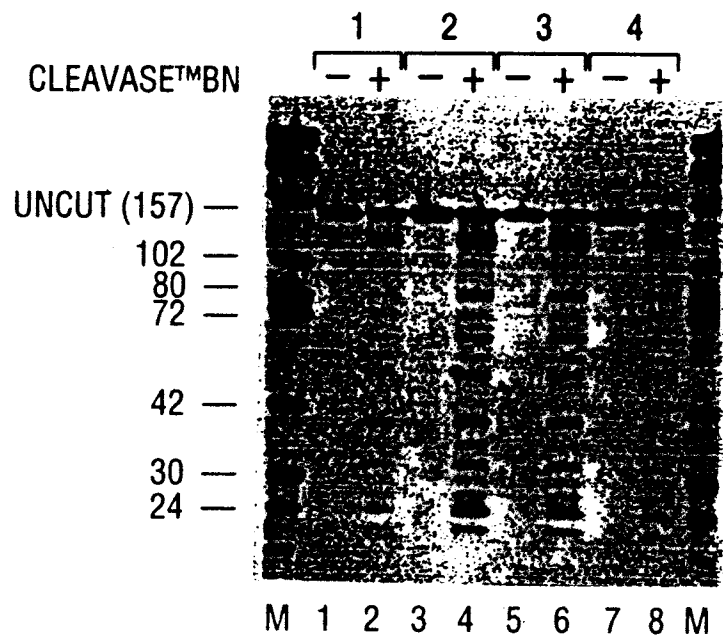


FIG. 33

**FIG. 35**

**FIG. 36**

**FIG. 38**

**FIG. 39**

STRAND	5' - BIOTIN SENSE STRAND						5' - FLUORESCEIN ANTI-SENSE STRAND					
	WT	419	422	WT	419	422	WT	419	422	WT	419	422
ssDNA												
250 ^{ng} BN	-	-	-	+	+	+	+	+	+	-	-	-
M	1	2	3	4	5	6	7	8	9	10	11	12

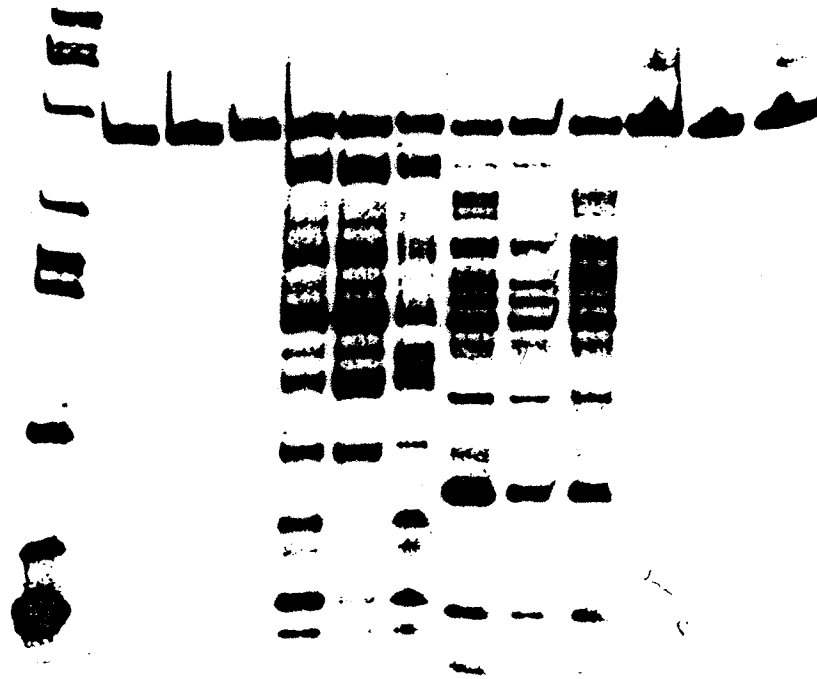


FIG. 40

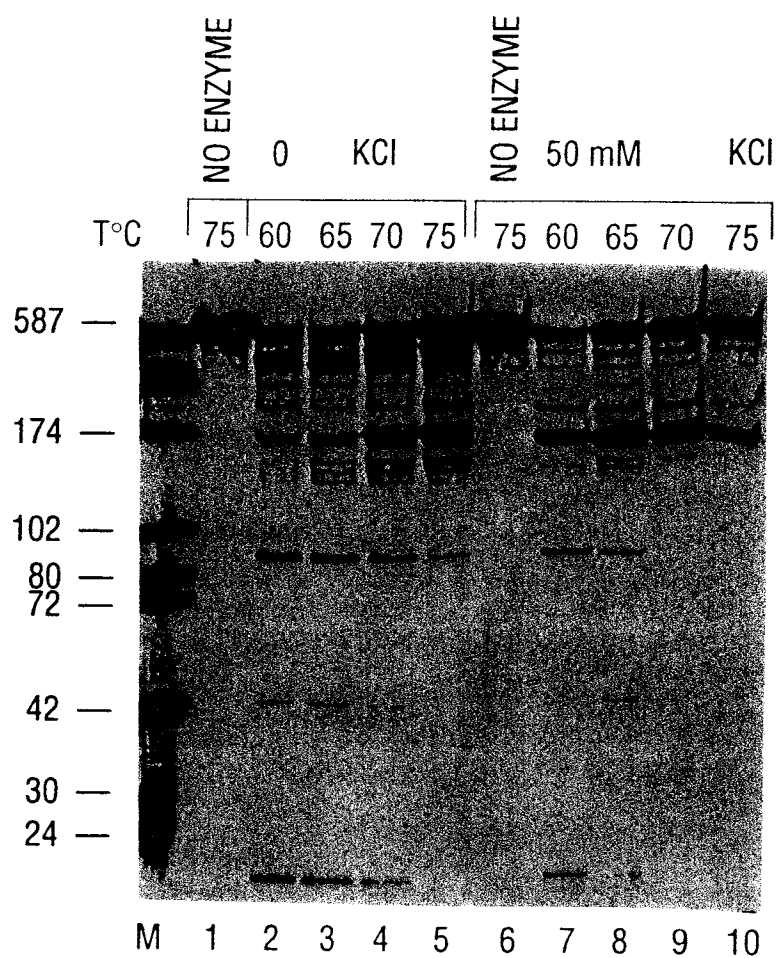


FIG. 41

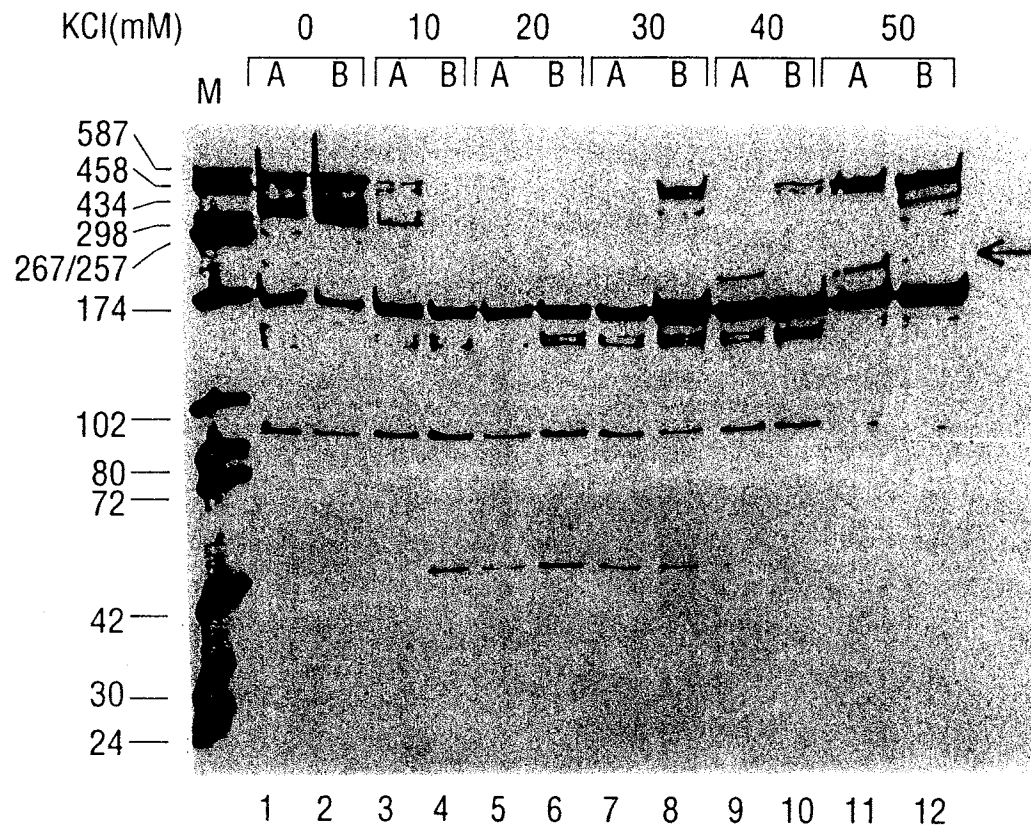


FIG. 42

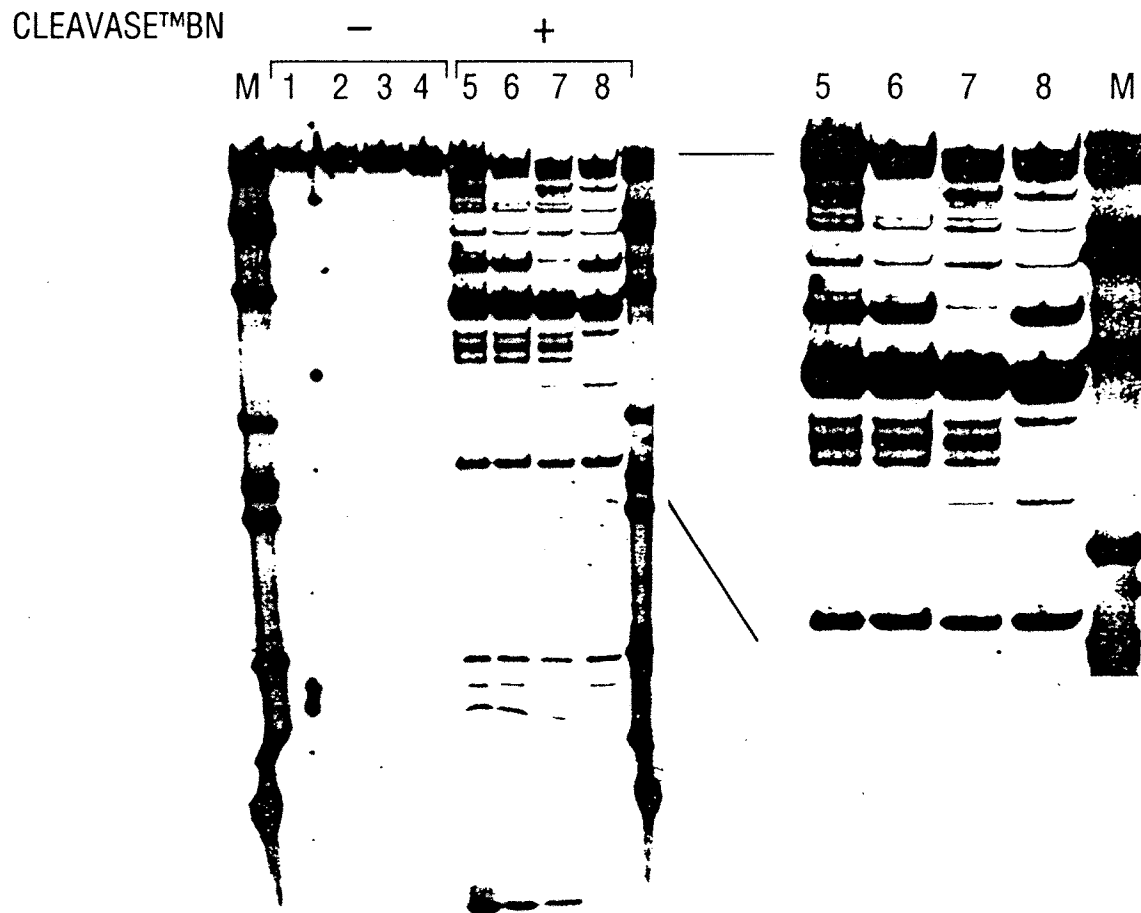


FIG. 43

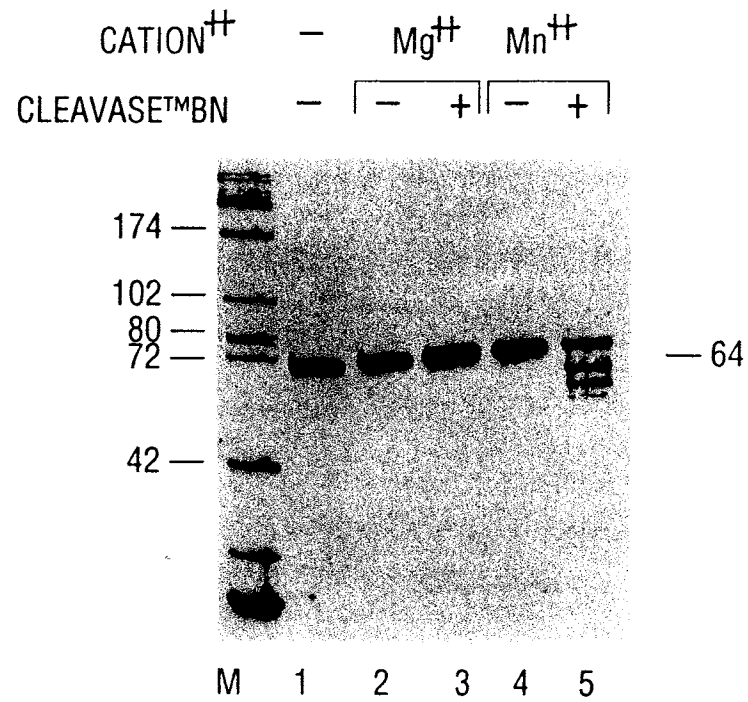


FIG. 44

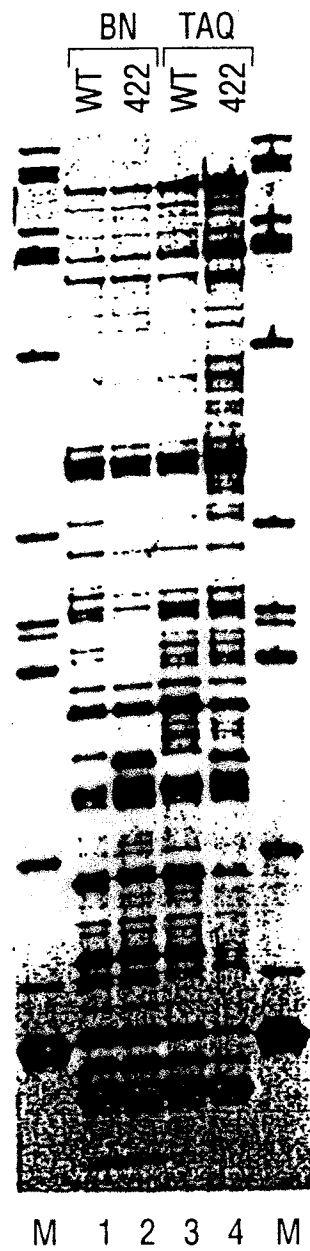


FIG. 45

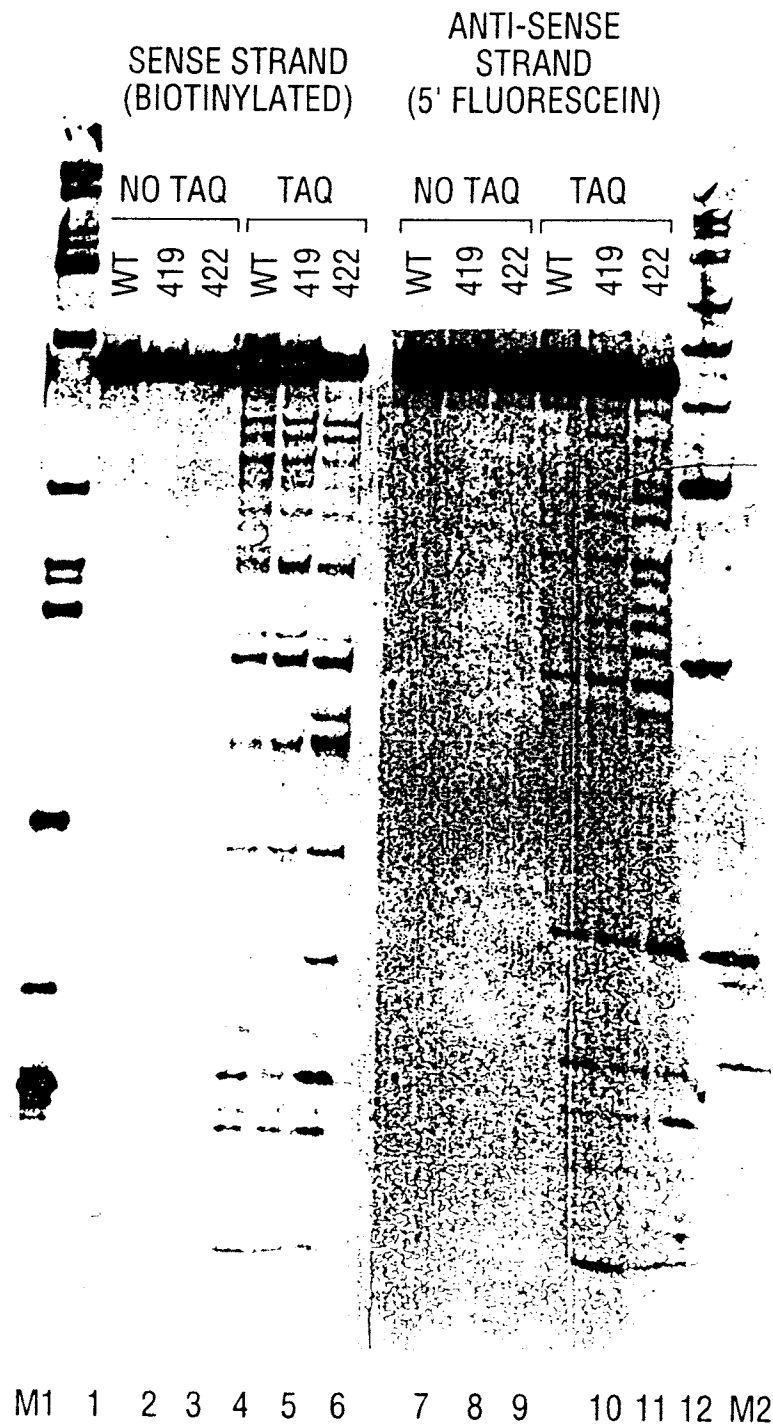
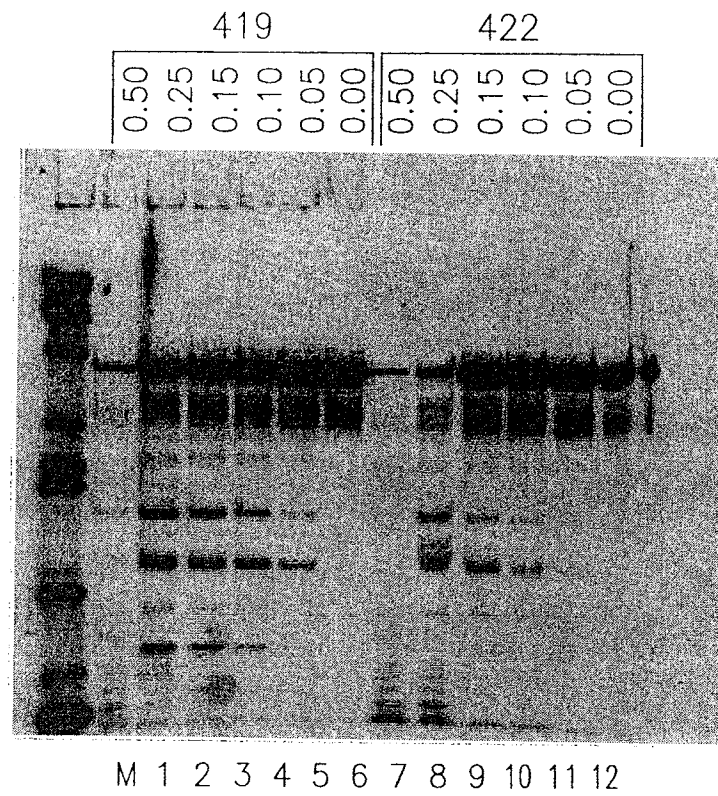


FIG. 46

**FIG. 47**

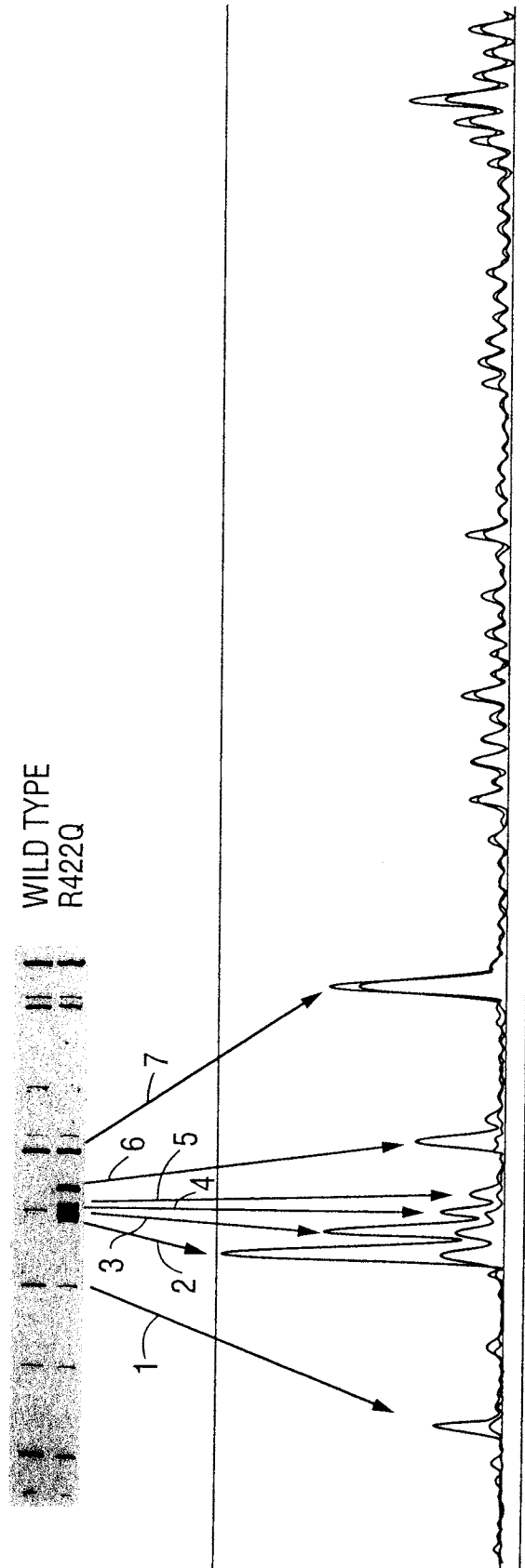


FIG. 48

L. 100.8-1 5'GGCTGACCAAGGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 76) 3'CCGACTGTTCTTCTTTGAGCGACTCTGTCGTCCCTGAAGAAGGTGTTCCCC

L. 46.16-10 5'GGCTGACCAAGGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 77) 3'CCGACTGTTCTTCTTTGAGCGACTCTATCGTCCCTGAAGAAGGTGTTCCCC

L. 46.16-12 5'GGCTGACCAAGGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 78) 3'CCGACTGTTCTTCTTTGAGCGACTCTATCGTCCCTGAAGAAGGTGTTCCCC

L19.16-3 5'GGCTGACCAAGGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 79) 3'CCGACTGTTCTTCTTTGAGCGACTCTGTCCCTGAAGAAGGTGTTCCCC

L. CEM/251 5'GGCTGACCAAGGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 80) 3'CCGACTGTTCTTCTTTGAGCGACTTTGTGTCCTGAAAGGTGTTCCCC

L. 36.8-3 5'GGCTGACCAAGGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAGGGG
(SEQ ID NO: 81) 3'CCGACTGTTCTTCTTTGAGCGACTCTGTCCCTGAAGAAGGTGTTCCCC

FIG. 49A

L. 100.8-1 (SEQ ID NO: 76)	ATGTTACGGGGAGGTA TACTGGGGAGGAGCCGGT CGGGAAACGCCCACTCTCT TACAATGCCCCCTCCATGACCCCTCCTCGGGCAGCCCTTGCGGGTGAGAGA	100
L. 46.16-10 (SEQ ID NO: 77)	ATGTTATGGGGAGG -----AGCCGGTCGGGAACACCCACTTTCT TACAATACCCCTCC -----TCGGCCAGCCCTTGTTGGGTGAAGA	
L. 46.16-12 (SEQ ID NO: 78)	ATGTTATGGGGAGG -----AGCCGGTCGGGAACACCCACTTTCT TACAATACCCCTCC -----TCGGCCAGCCCTTGTTGGGTGAAGA	
L19.16-3 (SEQ ID NO: 19)	ATGTTACGGGGAGGTA TACTGGGGAGGAGCCGGT CGGGAAACGCCCACTTTCT TACAATGCCCCCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGGAGAGA	
L. CEM/251 (SEQ ID NO: 80)	ATGTTACGGGGAGGTA TACTGGGAAGGAGCCGGT CGGGAAACGCCCACTTTCT TACAATGCCCCCTCCATGACCCCTTCTCGGCCAGCCCTTGCGGGTGAAAGA	
L. 36.8-3 (SEQ ID NO: 81)	ATGTTACGGAGAGGTA TCTGGGGAGGAGCCGGT CGGGAAACGCCCACTTTCT TACAATGCCCTCTCCATGACCCCTCCTCGGCCAGCCCTTGCGGGTGAGAGA	

FIG. 49B

150
L. 100.8-1
5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGGGA
3' ACTACATATTTATAGTGACCGTAAAGCGAGACATAAGTCAGCGAGACGCCCT
L. 46.16-10
5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGGGA
3' ACTACATATTTATAGTGACCGTAAAGCGAGACATAAGTCAGCGAGACGCCCT
L. 46.16-12
5' TGGTGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGGGA
3' ACCACATATTTATAGTGACCGTAAAGCGAGACATAAGTCAGCGAGACGCCCT
L. 19.16-3
5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGGGA
3' ACTACATATTTATAGTGACCGTAAAGCGAGACATAAGTCAGCGAGACGCCCT
L. CEM/251
5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGGGA
3' ACTACATATTTATAGTGACCGTAAAGCGAGACATAAGTCAGCGAGACGCCCT
L. 36.8-3
5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAGTCGCTCTGGGA
3' ACTACATATTTATAGTGACCGTAAAGCGAGACATAAGTCAGCGAGACGCCCT

FIG. 49C

L.100.8-1

200
GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCCTTAACCTCGGGACCCCTCCAAGAGAGGTGATCGTCCATC

L.46.16-10

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGCTAG
CTCCGACCCTTAACCTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.46.16-12

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCCTTAACCTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.19.16-3

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCCTTAACCTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.CEM/251

GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCCTTAACCTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.36.8-3

GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCCTTAACCTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC

FIG. 49D

L. 100. 8 -1	5'AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGC	ACTTG	GGCCGGT	GCTGGG	250
(SEQ ID NO: 76)	3'TCGGACCCACAAGG	ACCATTCTG	AGAGTGGT	CGTGA	ACC	GGCCACGACCC
L. 46.16-10	5'AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGC	ACTTAG	CCAGT	GCTGGG	
(SEQ ID NO: 77)	3'TCGGACCCACAAGG	ACGATCTG	AGAGTGGT	CGTGA	ATCGGT	CACGACCC
L. 46.16-12	5'AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGC	ACTTG	GGCCAGT	GCTGGG	
(SEQ ID NO: 78)	3'TCGGACCCACAAGG	ACGATCTG	AGAGTGGT	CGTGA	ACCGGTC	ACGACCC
L. 19.16-3	5'AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGC	ACTTG	GGCCGGT	GCTGGG	
(SEQ ID NO: 79)	3'TCGGACCCACAAGG	ACGATCTG	AGAGTGGT	CGTGA	ACCGGCC	CACGACCC
L. CEM/251	5'AGCCTGGGTGTTCCCTGCTAGAC	TCTCACCAGC	ACTTG	GGCCGGT	GCTGGG	
(SEQ ID NO: 80)	3'TCGGACCCACAAGG	ACGATCTG	AGAGTGGT	CGTGA	ACCGGCC	CACGACCC
L. 36.8-3	5'AGCCTGAGTGTTCCTGCTAAAC	TCTCACCAGC	ACTTG	GGCCGGT	GCTGGG	
(SEQ ID NO: 81)	3'TCGGACTCACCAAGG	ACGATTTG	AGAGTGGT	CGTGA	ACCGGCC	CACGACCC

HAIRPIN

FIG. 49E

L. 100. 8 -1 (SEQ ID NO: 76)	CAGAGTGGCTCCACGCTTGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCACCAGAGGTGCCGAACGAACGAATTTCTGGAGAAGTTATTTCCGACCGC	300
L. 46.16-10 (SEQ ID NO: 77)	CAGAGTGGCTCCACGCTTGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCACCAGAGGTGCCGAACGAACGAATTTCTGGAGAAGTTATTTCCGACCGG	
L. 46.16-12 (SEQ ID NO: 78)	CAGAGTGGCTCCACGCTTGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCACCAGAGGTGCCGAACGAACGAATTTCTGGAGAAGTTATTTCCGACCGG	
L. 19.16-3 (SEQ ID NO: 79)	CAGAGTGGCTCCACGCTTGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCACCAGAGGTGCCGAACGAACGAATTTCTGGAGAAGTTATTTCCGACCGG	
L. CEM/251 (SEQ ID NO: 80)	CAGAGTGACTCCACGCTTGCTTGCTTAAAGCCCTCTTCAATAAAGCTGCC GTCTCACCAGAGGTGCCGAACGAACGAATTTCTGGAGAAGTTATTTCCGACCGG	
L. 36.8-3 (SEQ ID NO: 81)	CAGAGCGGCTCCACGCTTGCTTGCTTAAAGACCTCTTCAATAAAGCTGCC GTCTCGCCGAGGTGCCGAACGAACGAATTTCTGGAGAAGTTATTTCCGACCGG	

HAIRPIN

FIG. 49F

L.100.8-1	5'ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATCCGGTCACACACAAGGGTAGAGAGGATCGGCCGGGAC	350 G 3' C 5'
L.46,16-10	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATTCGGTCACACACAAGGGTAGAGAGGATCGGCCGGGAC	G 3' C 5'
L.46.16-12	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATTCGGTCACACACAAGGGTAGAGAGGATCGGCCGGGAC	G 3' C 5'
L.19,16-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATCCGATCACACACAAGGGTAGAGAGGATCGGCCGGGAC	G 3' C 5'
L.CEM/251	5'ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATTCGATCACACACAAGGGTAGAGAGGATCGGCCGGGAC	G 3' C 5'
L.36.8-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATCCGATCACACACAAGGGTAGAGAGGATCGGCCGGGAC	G 3' C 5'

FIG. 49G

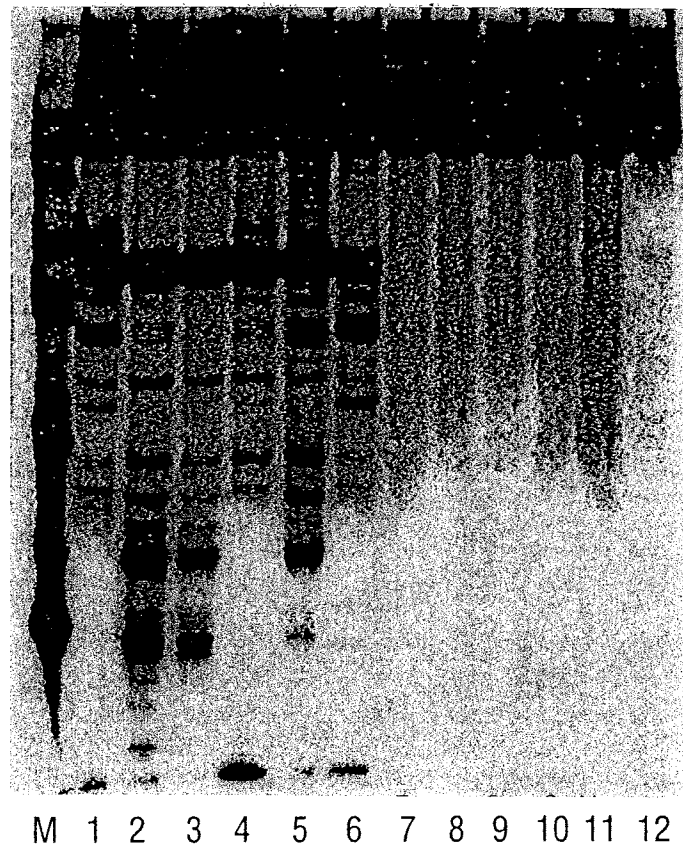


FIG. 50

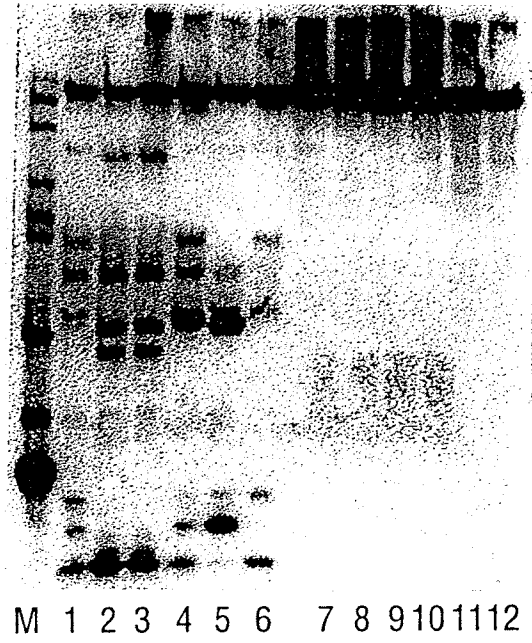


FIG. 51

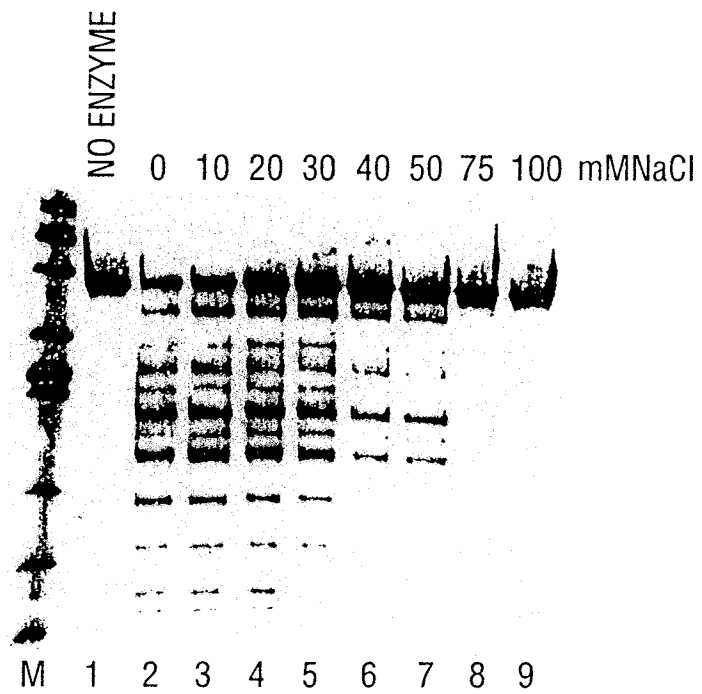


FIG. 52

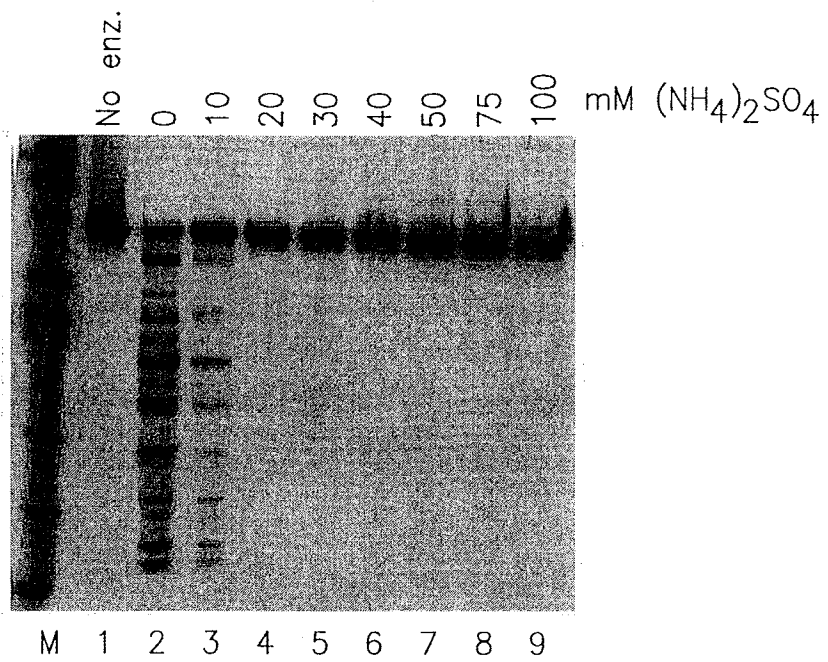


FIG. 53

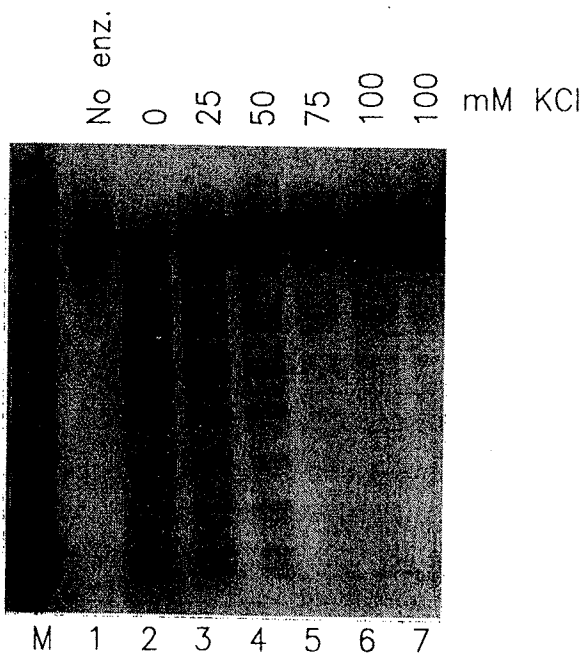


FIG. 54

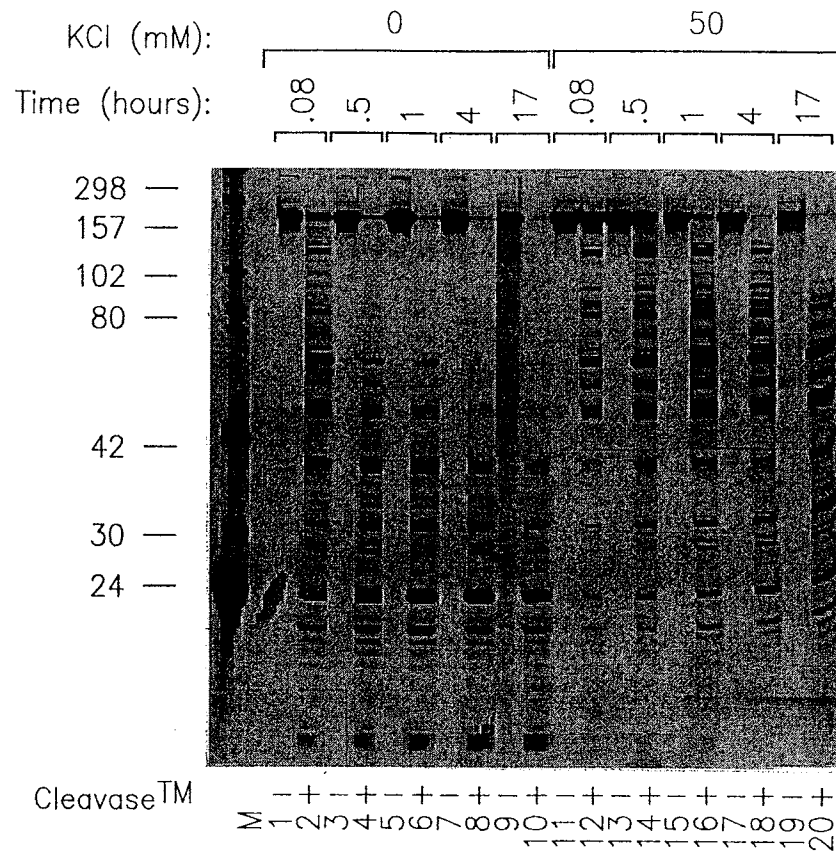


FIG. 55

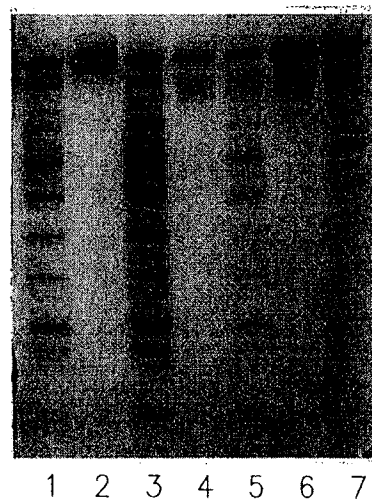


FIG. 56

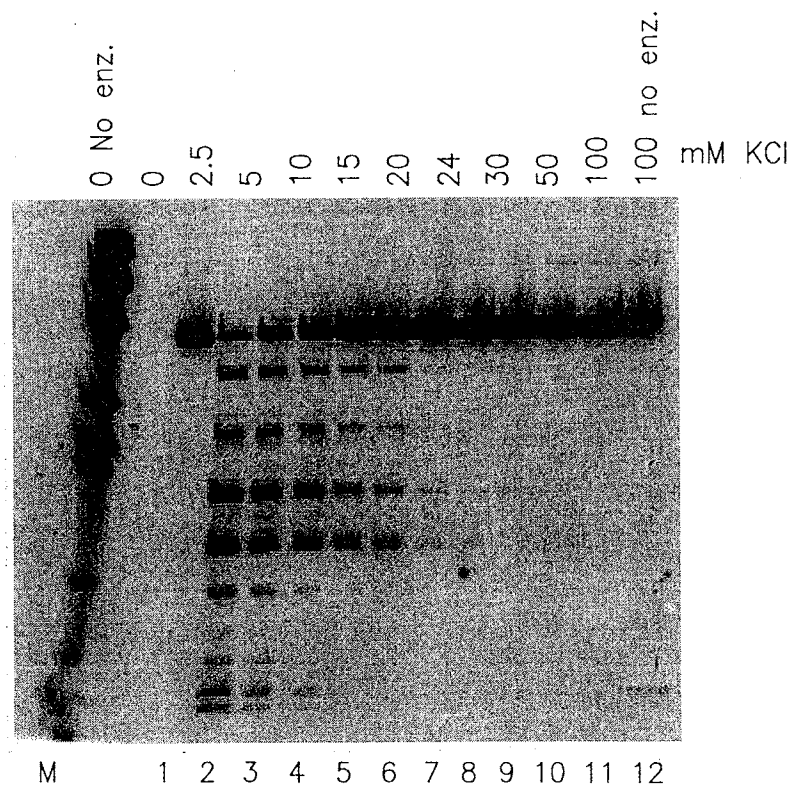


FIG. 57

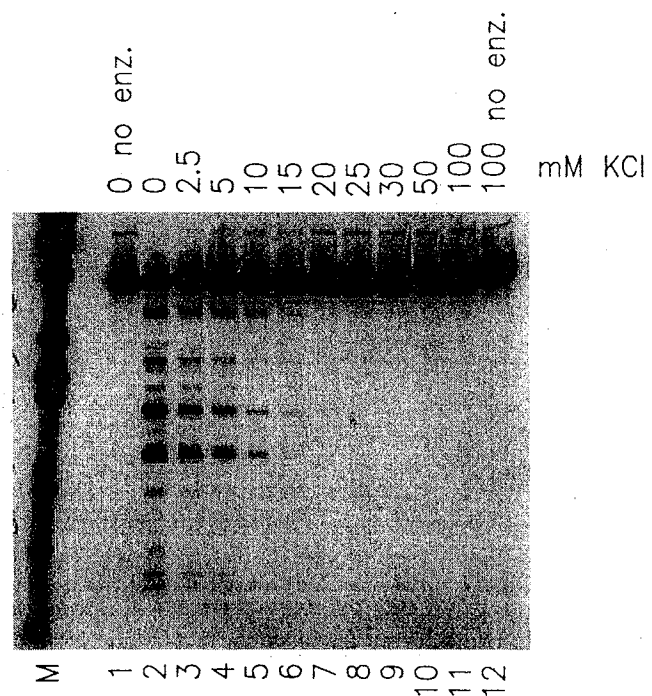


FIG. 58

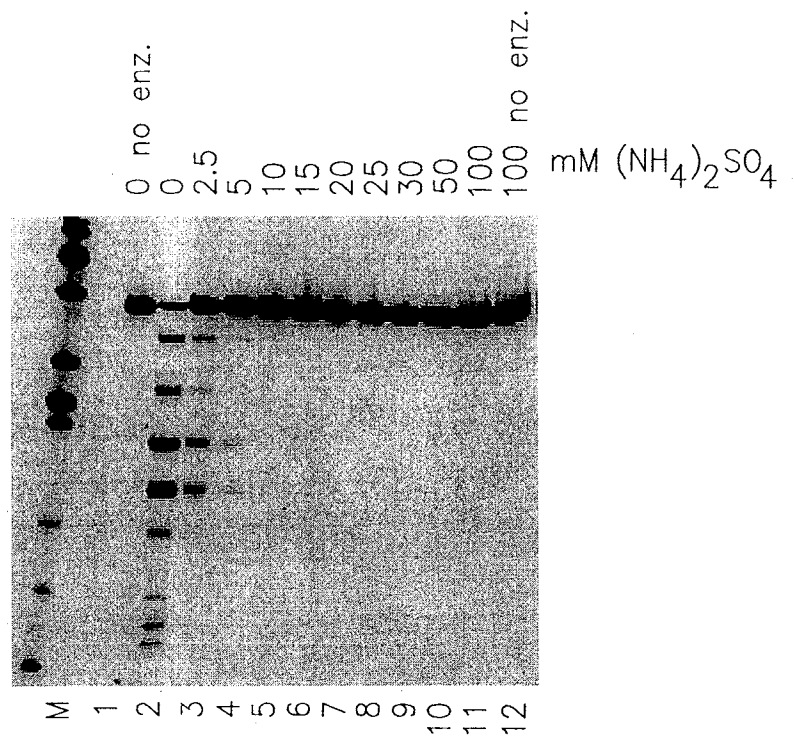


FIG. 59

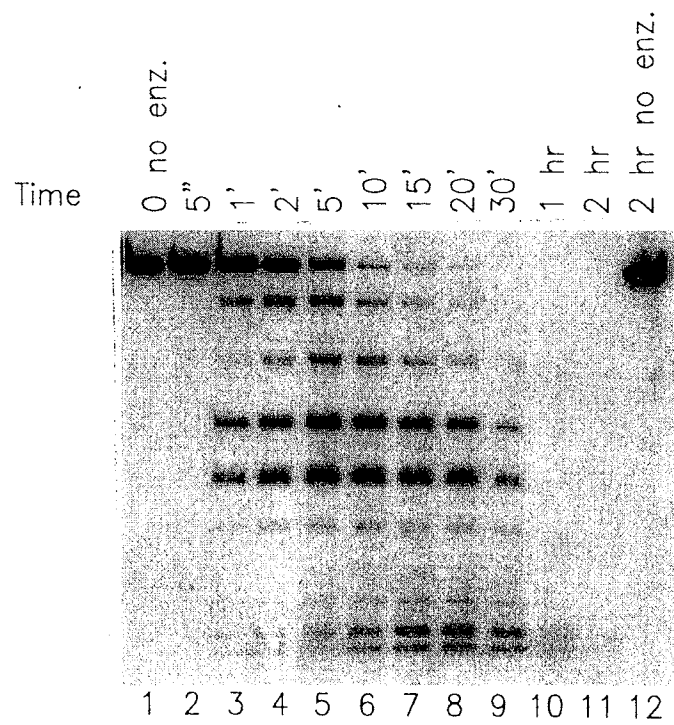


FIG. 60

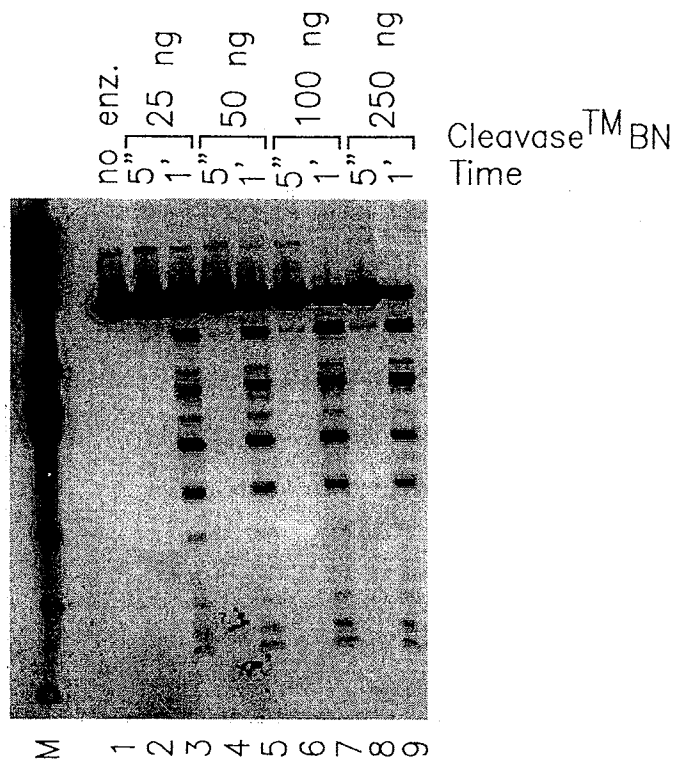


FIG. 61

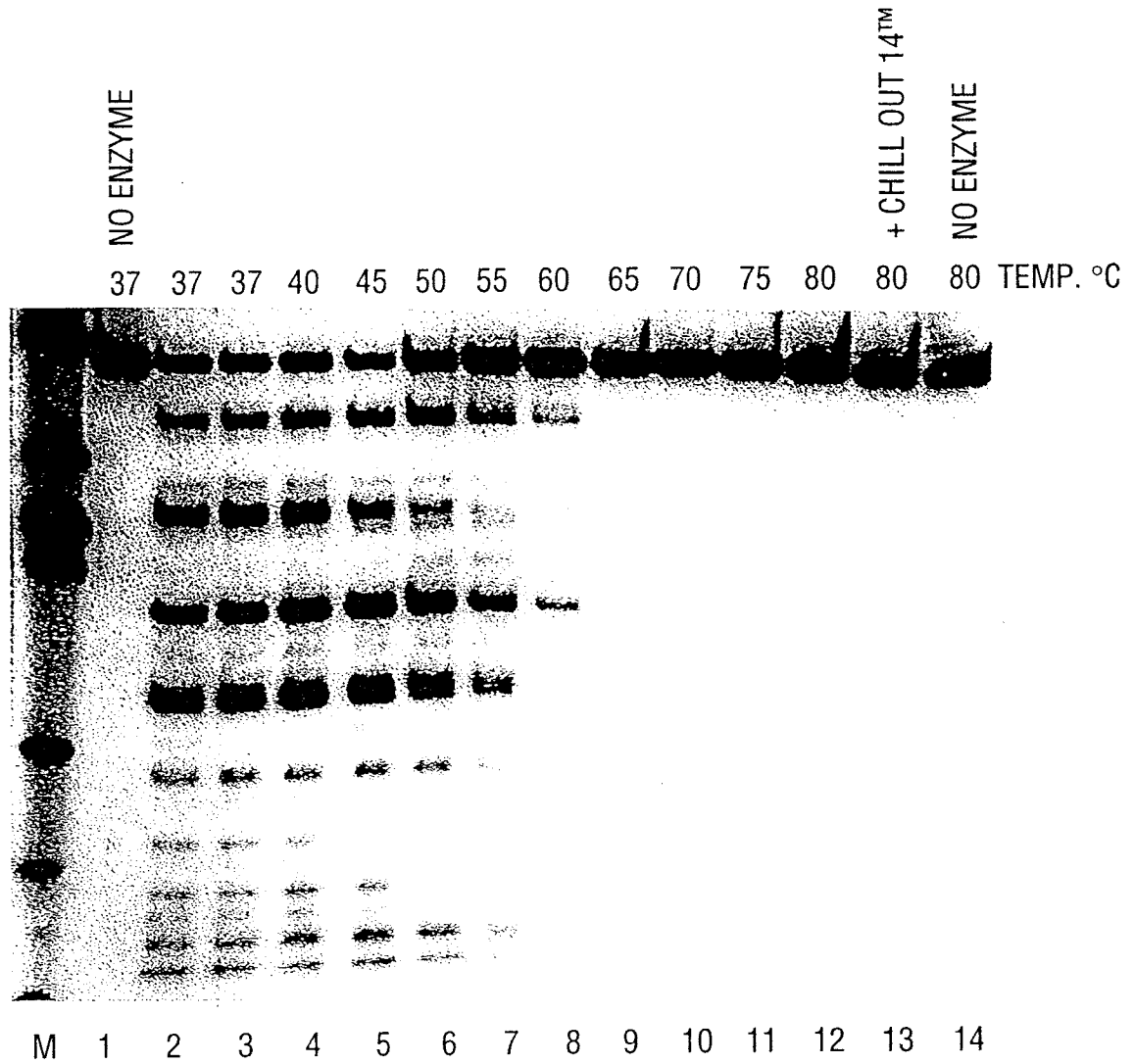


FIG. 62

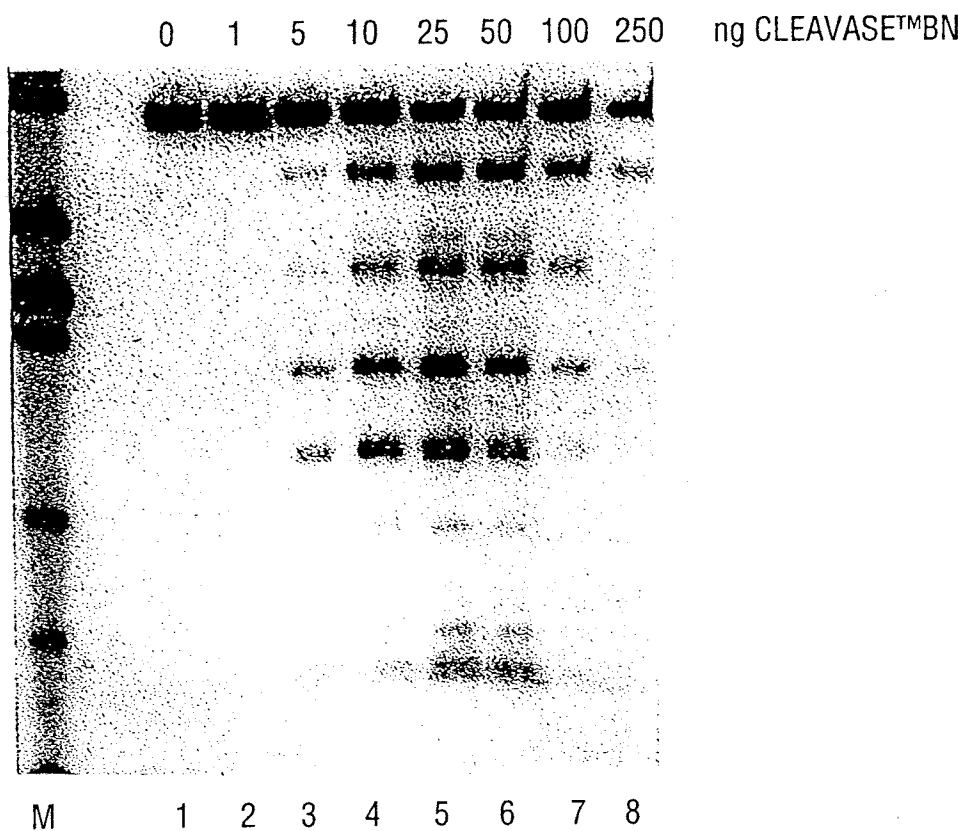


FIG. 63

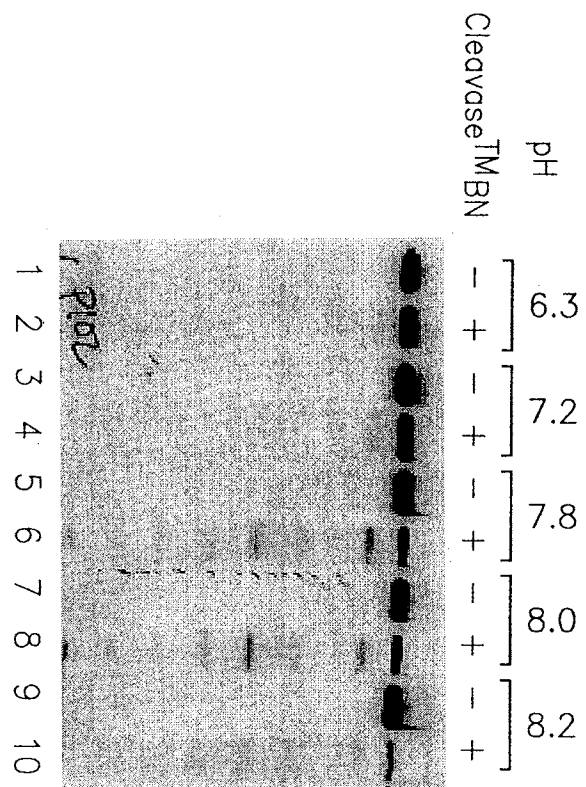


FIG. 64A

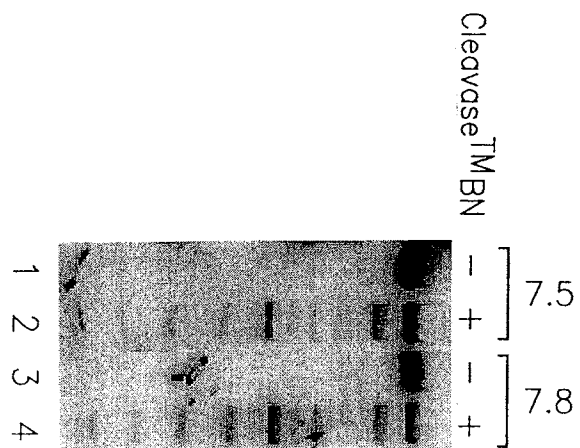


FIG. 64B

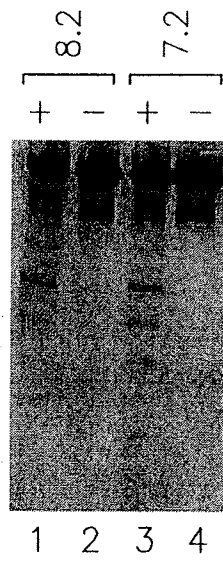


FIG. 65A

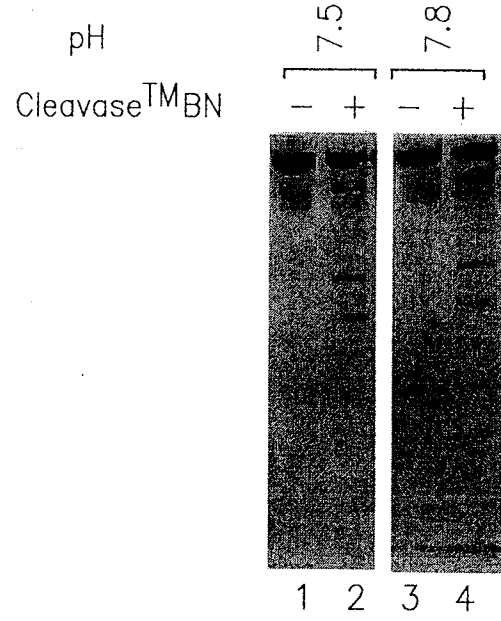


FIG. 65B

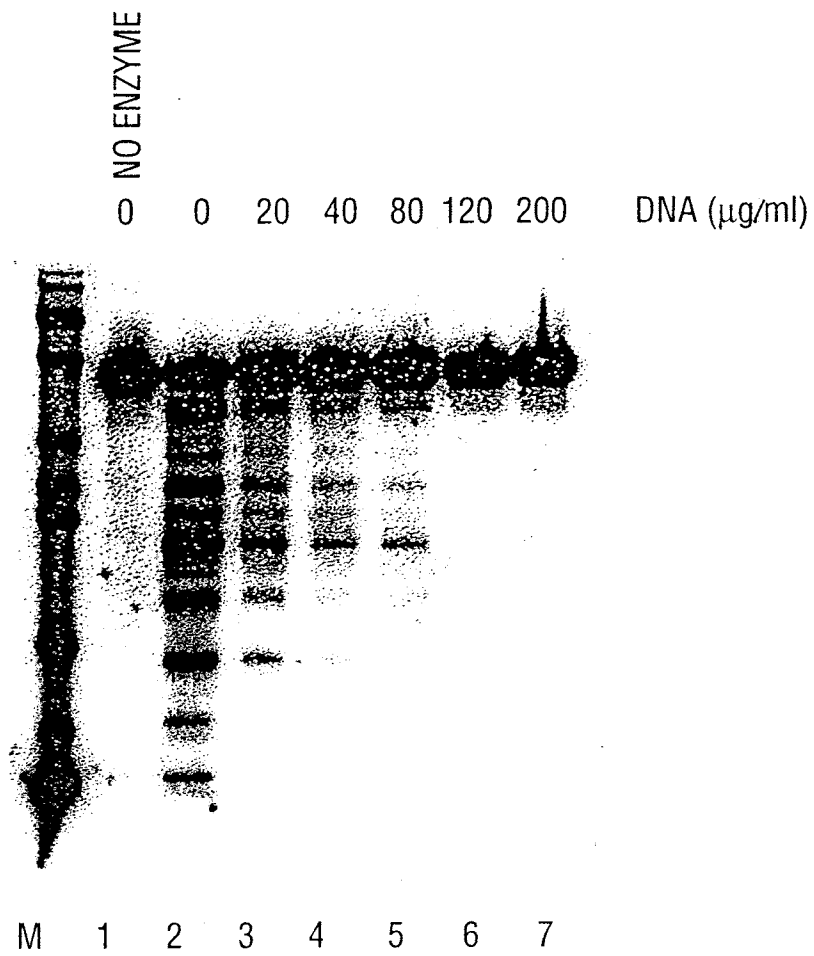
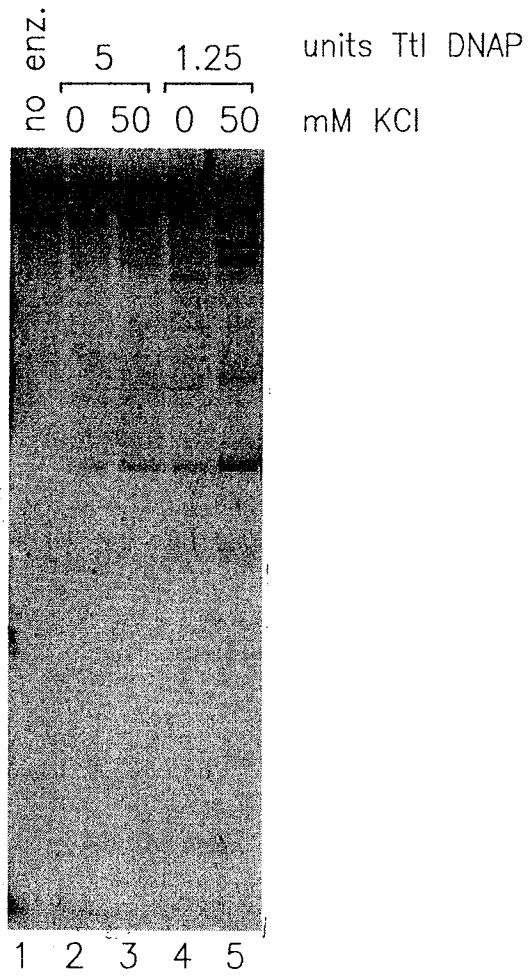
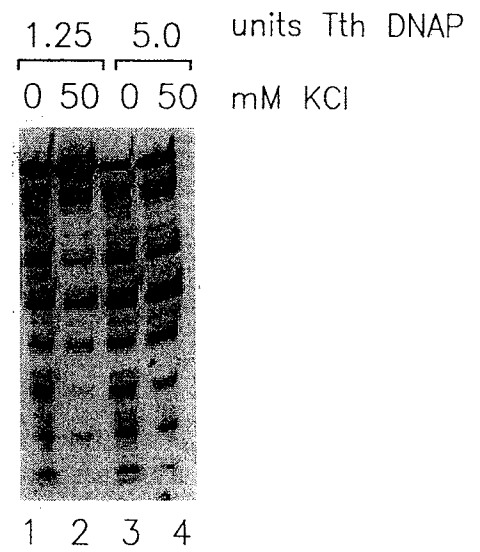


FIG. 66

**FIG. 67****FIG. 68**

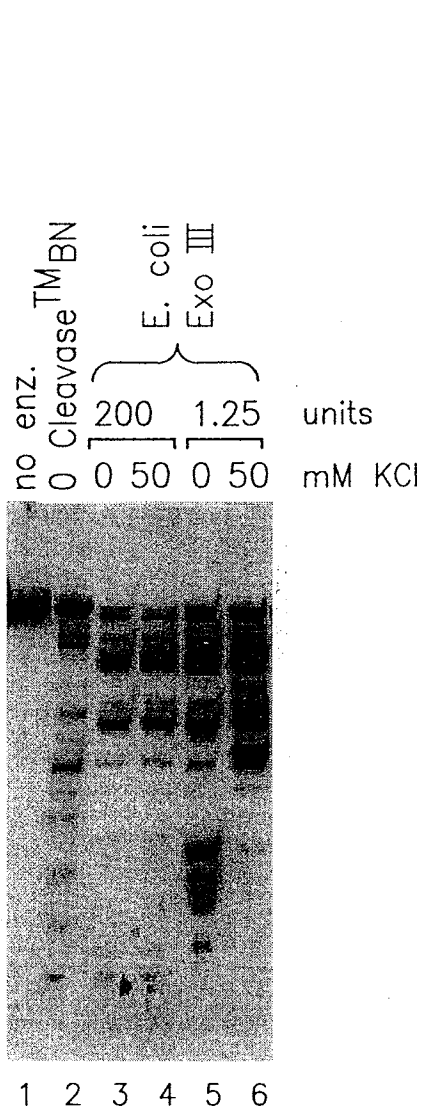


FIG. 69

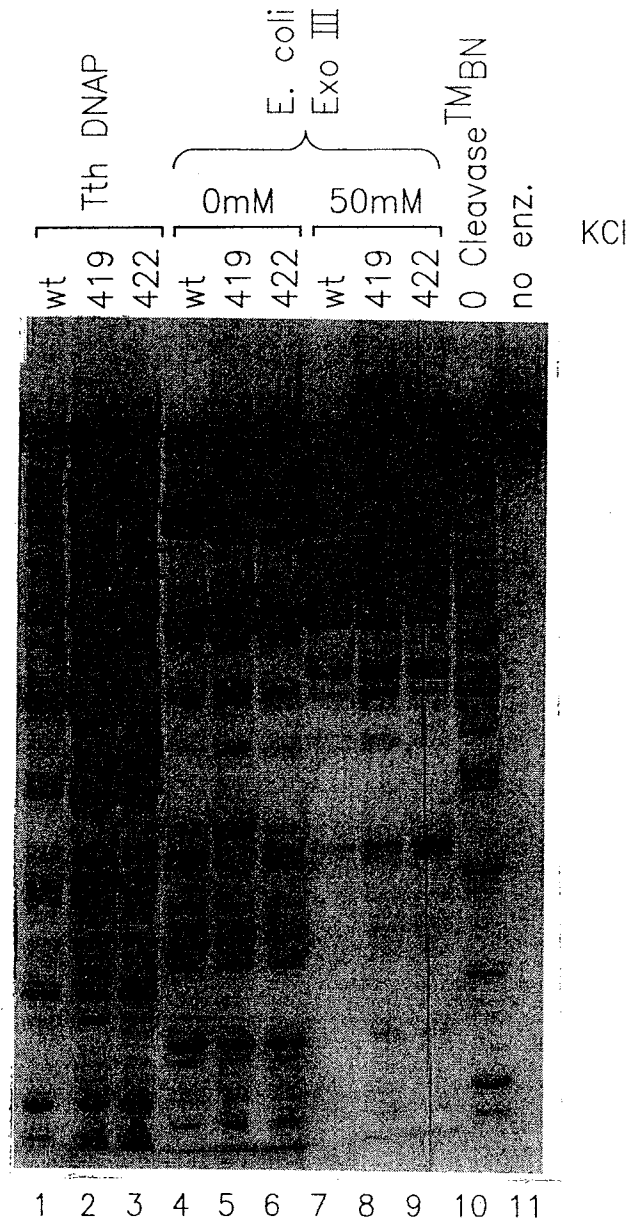
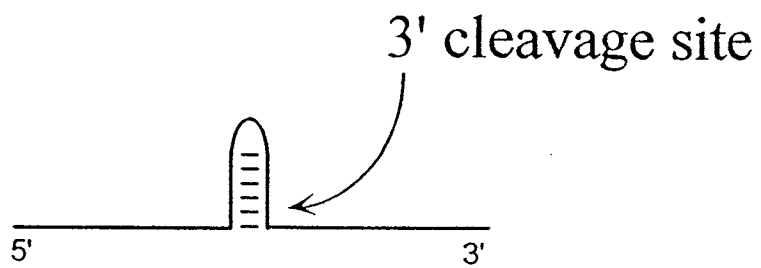
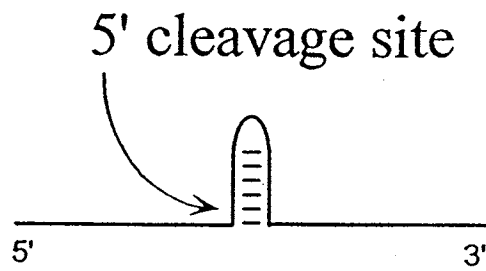


FIG. 70

FIG. 71



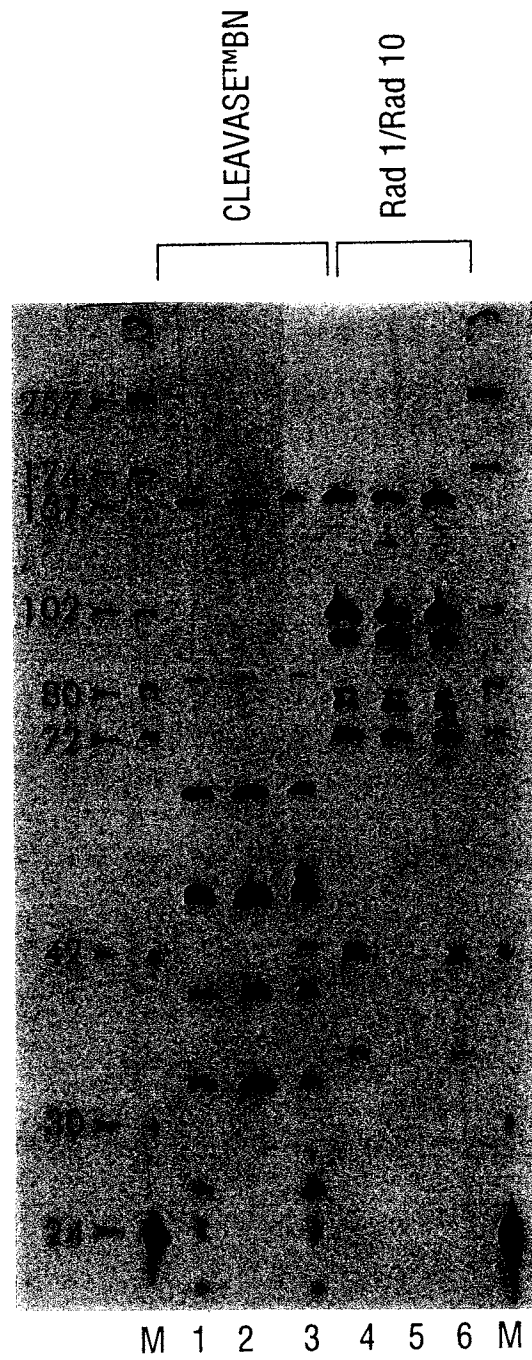


FIG. 72

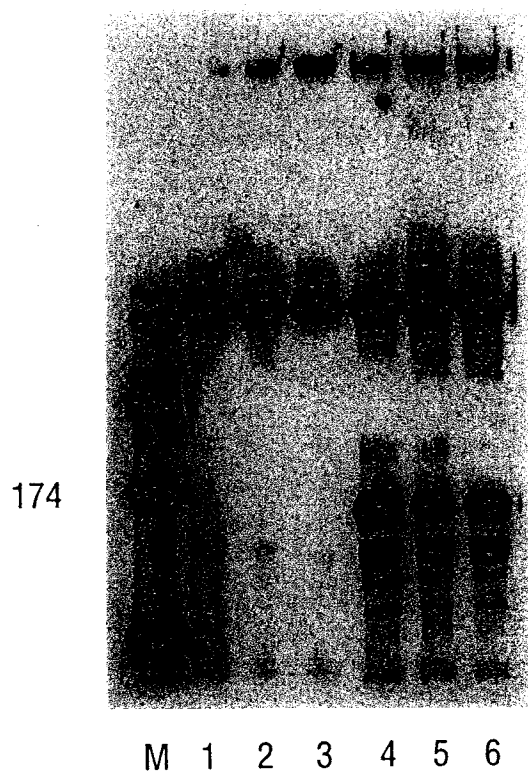


FIG. 73

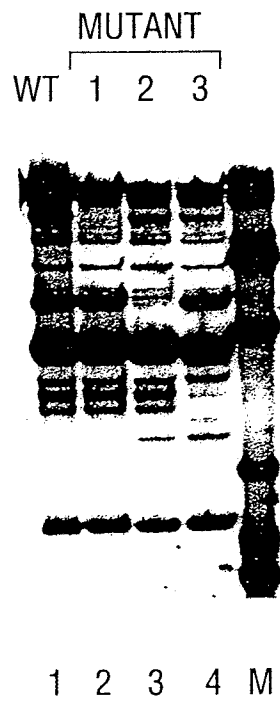


FIG. 74A

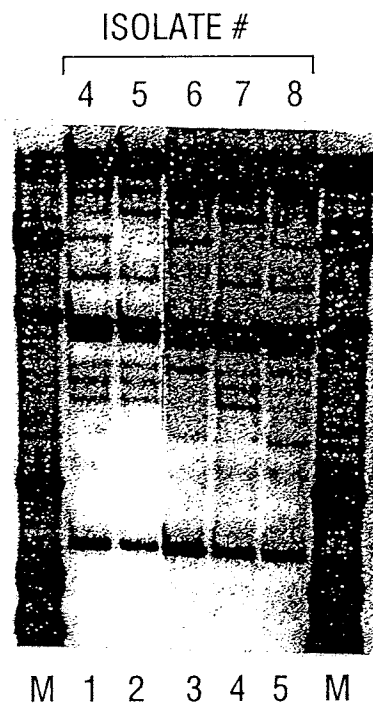


FIG. 74B

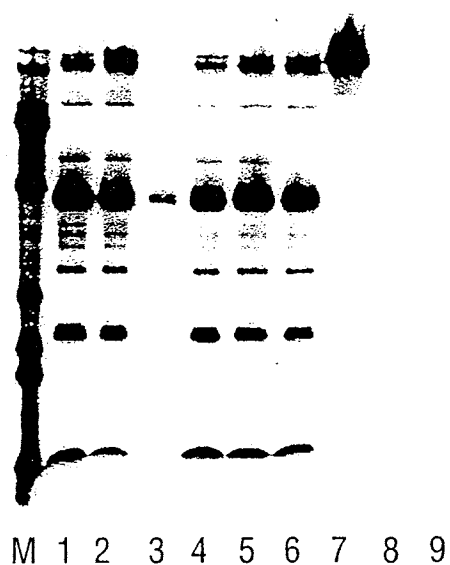


FIG. 75

% OF TOTAL
MUTATIONS

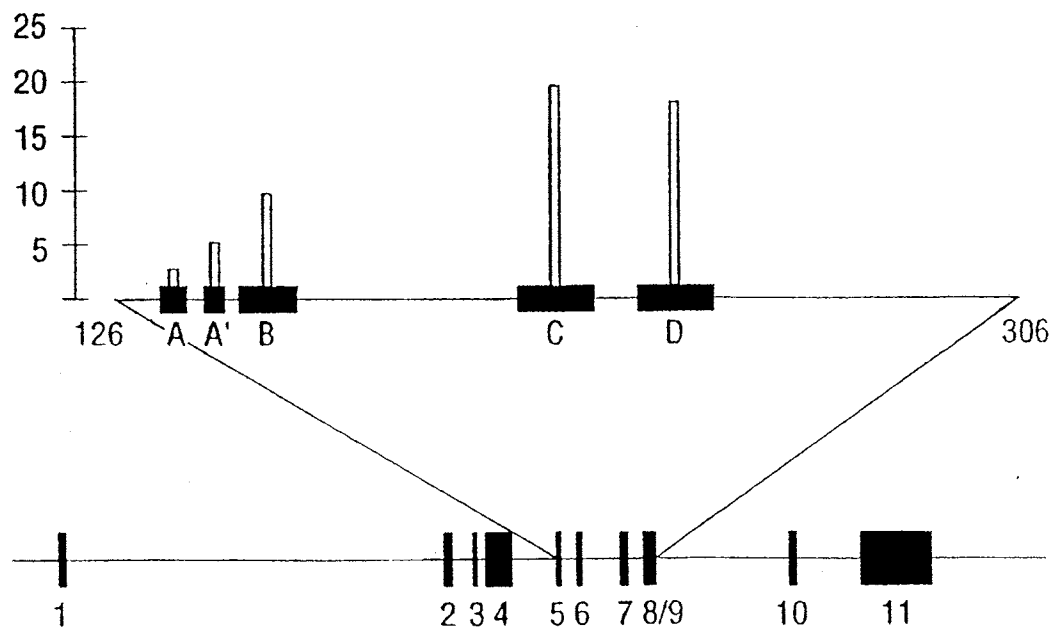


FIG. 76

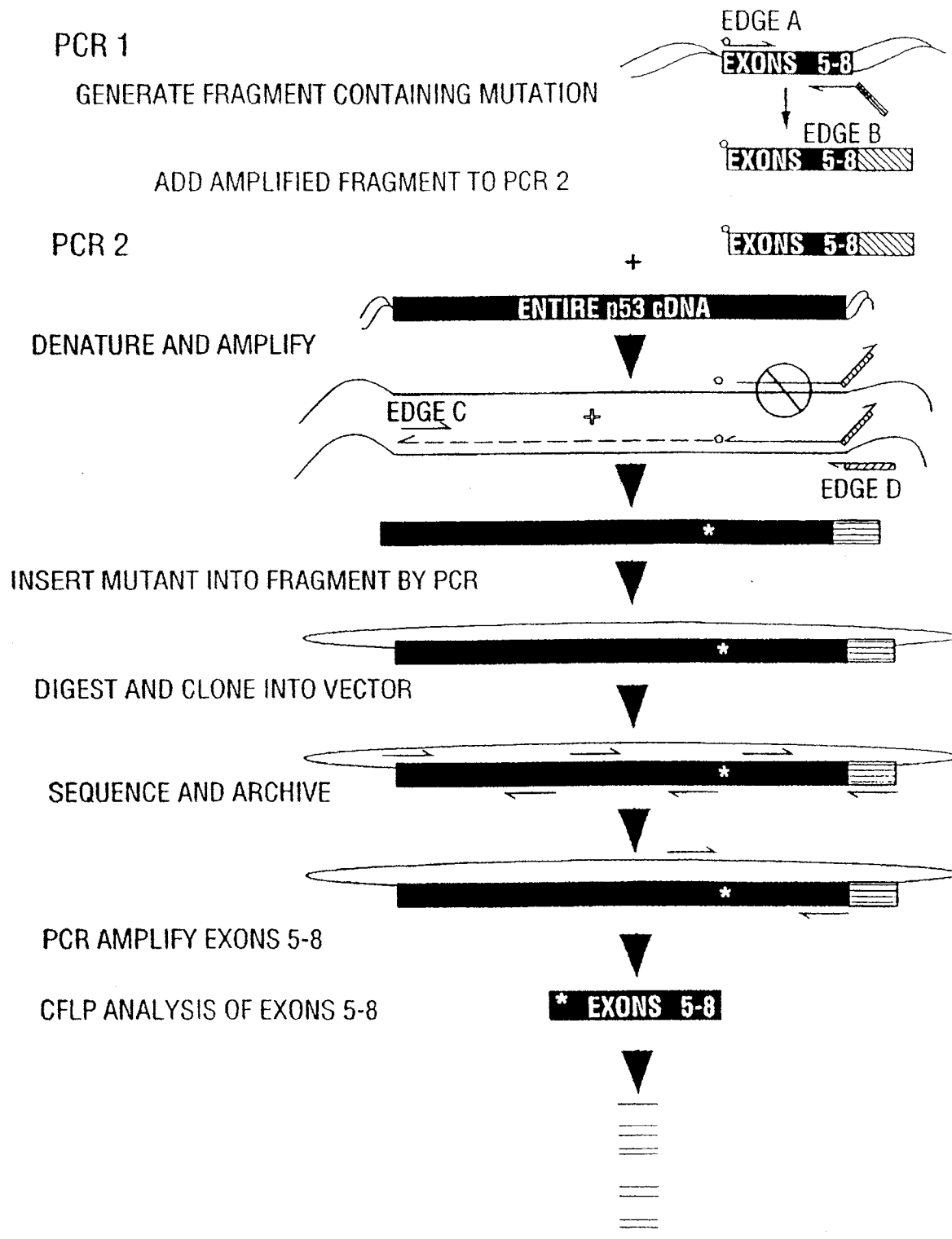


FIG. 77

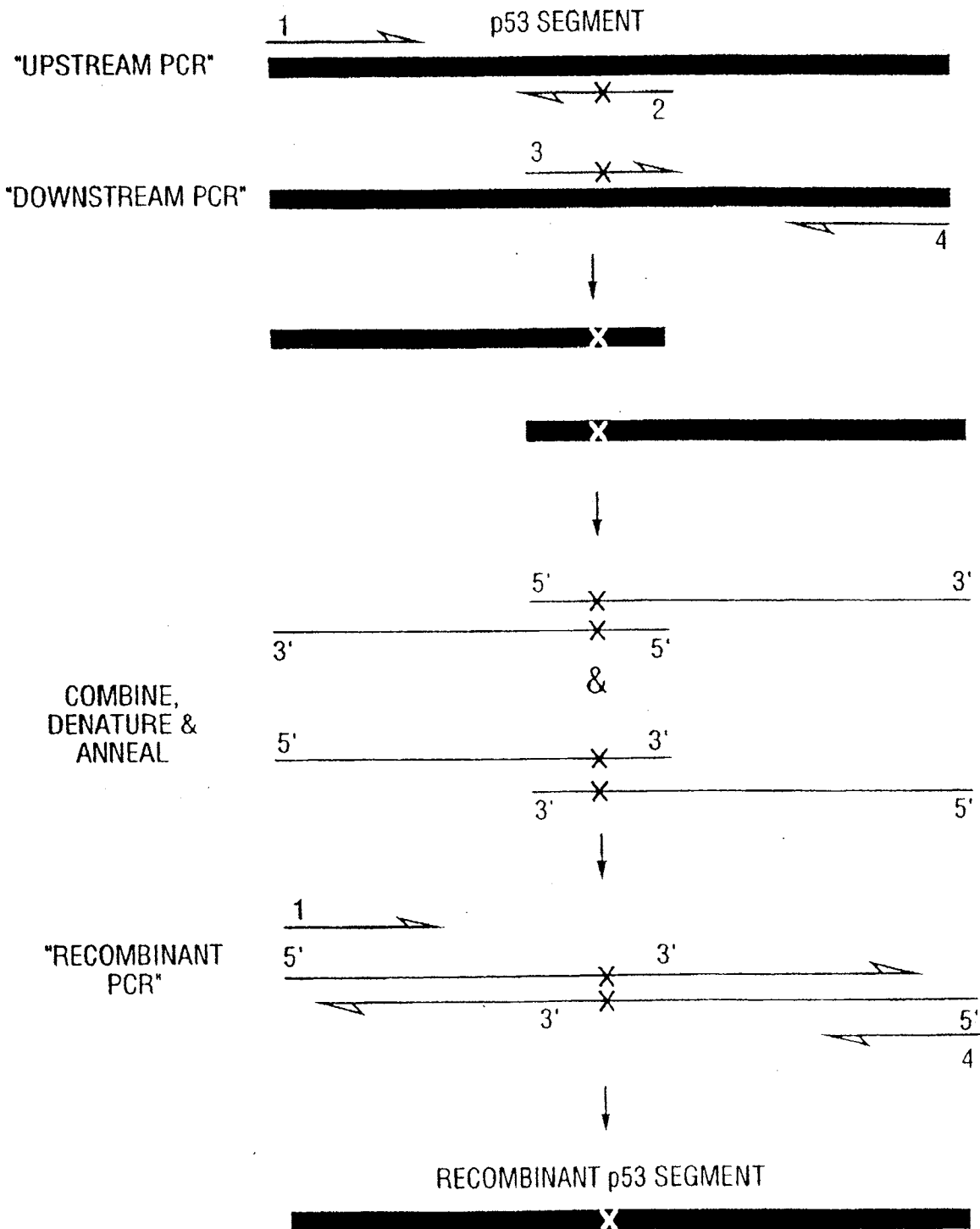


FIG. 78

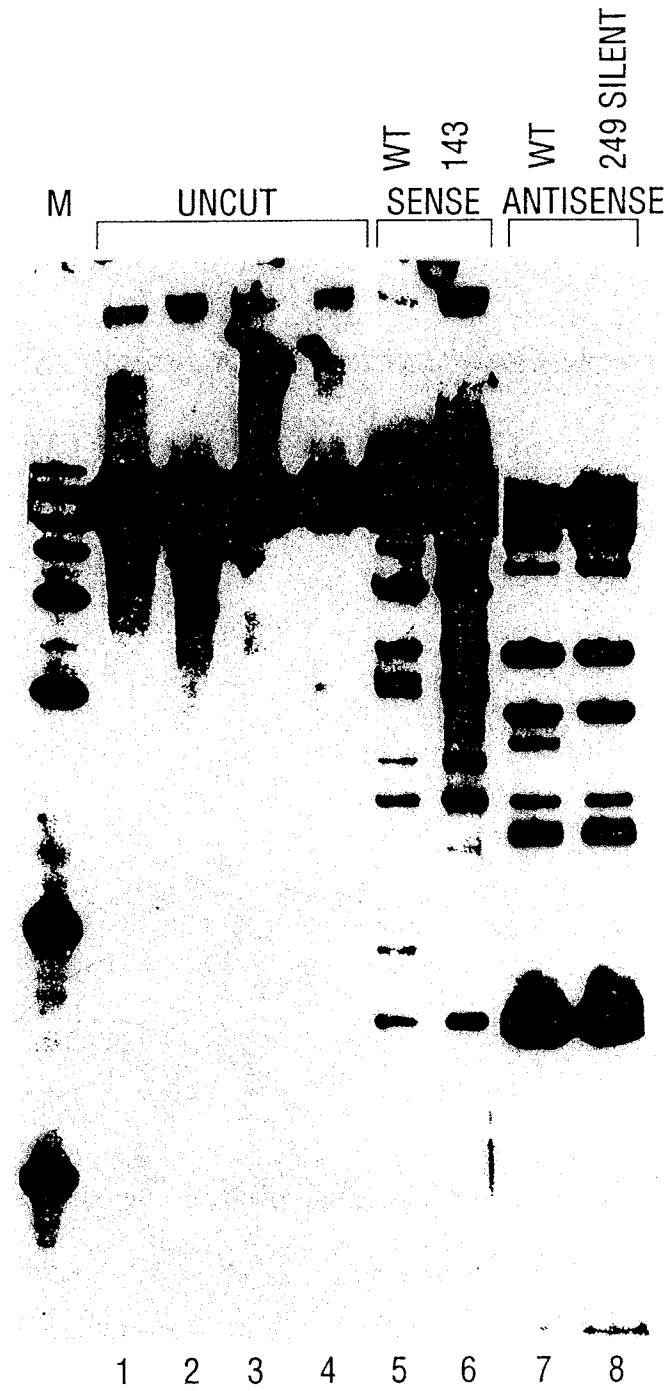


FIG. 79

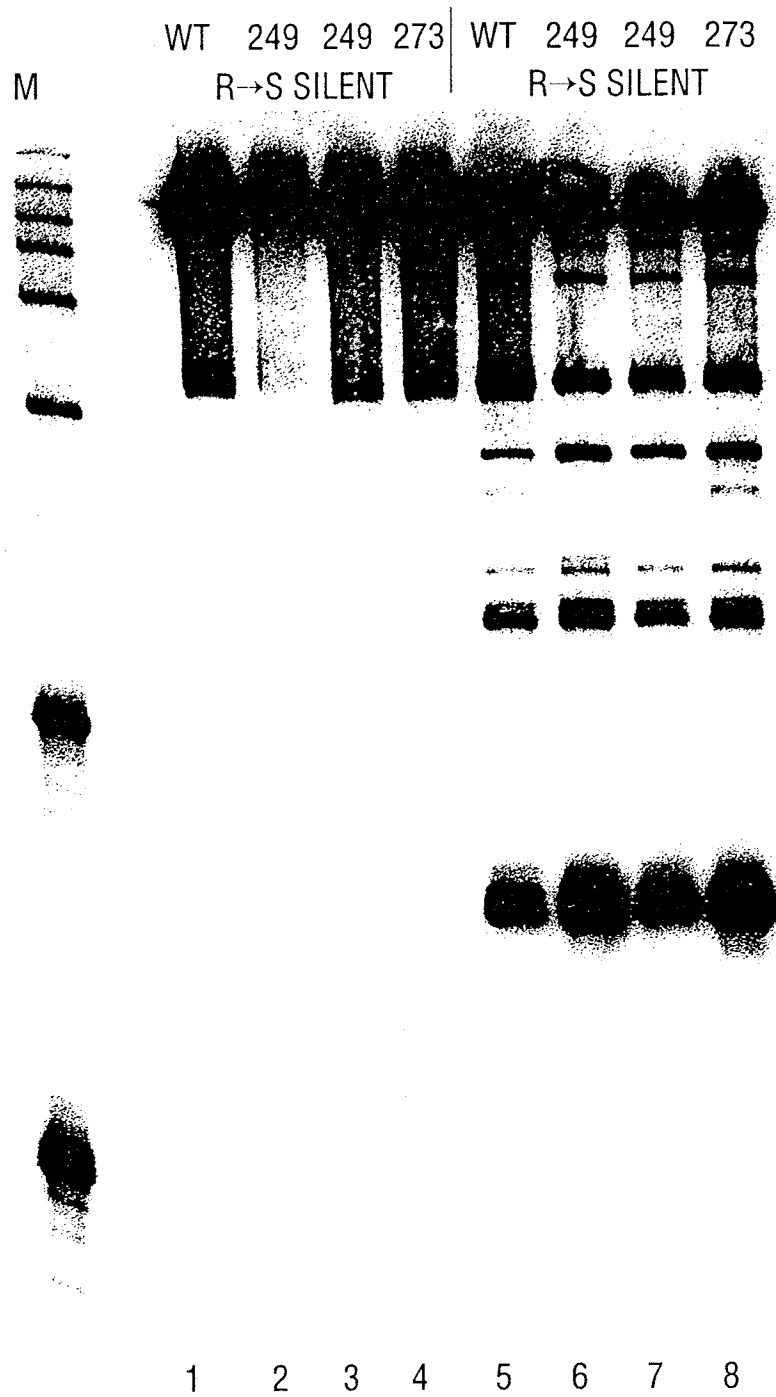


FIG. 80

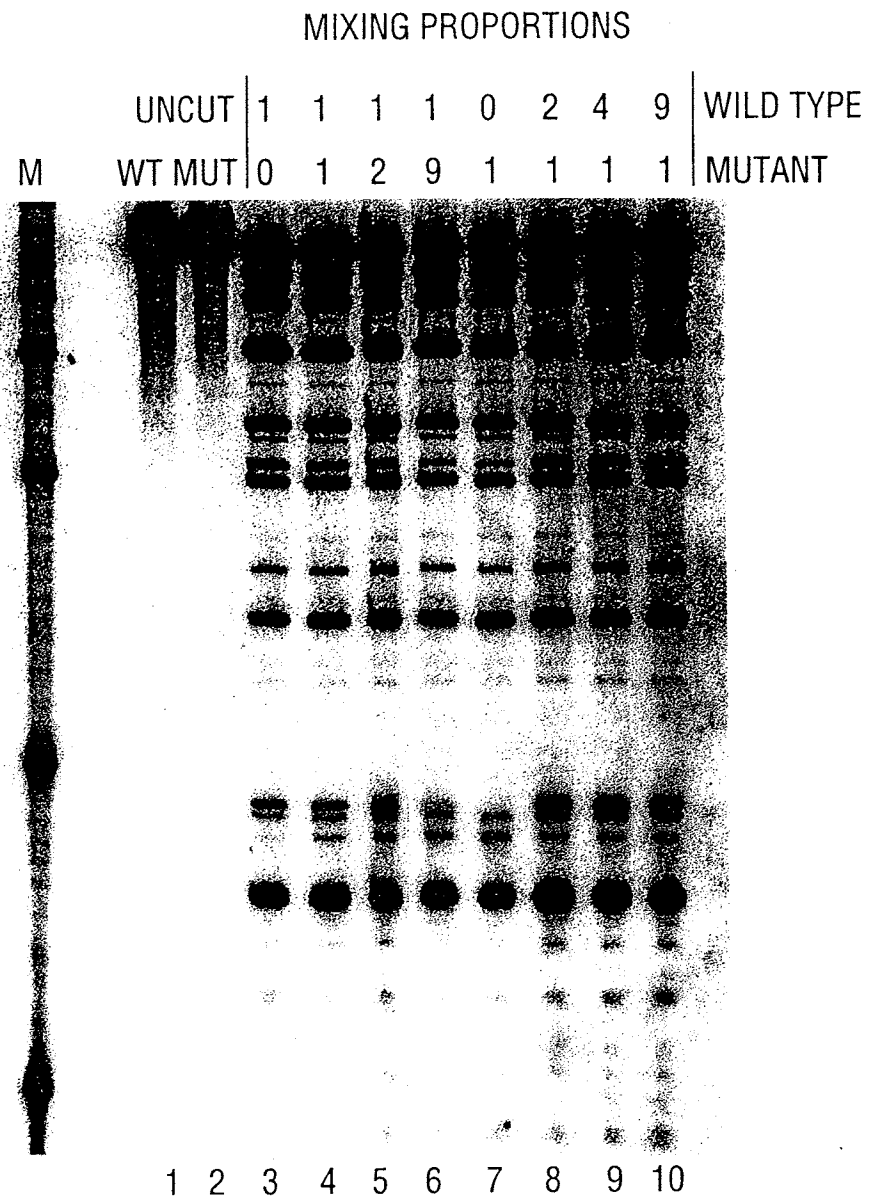
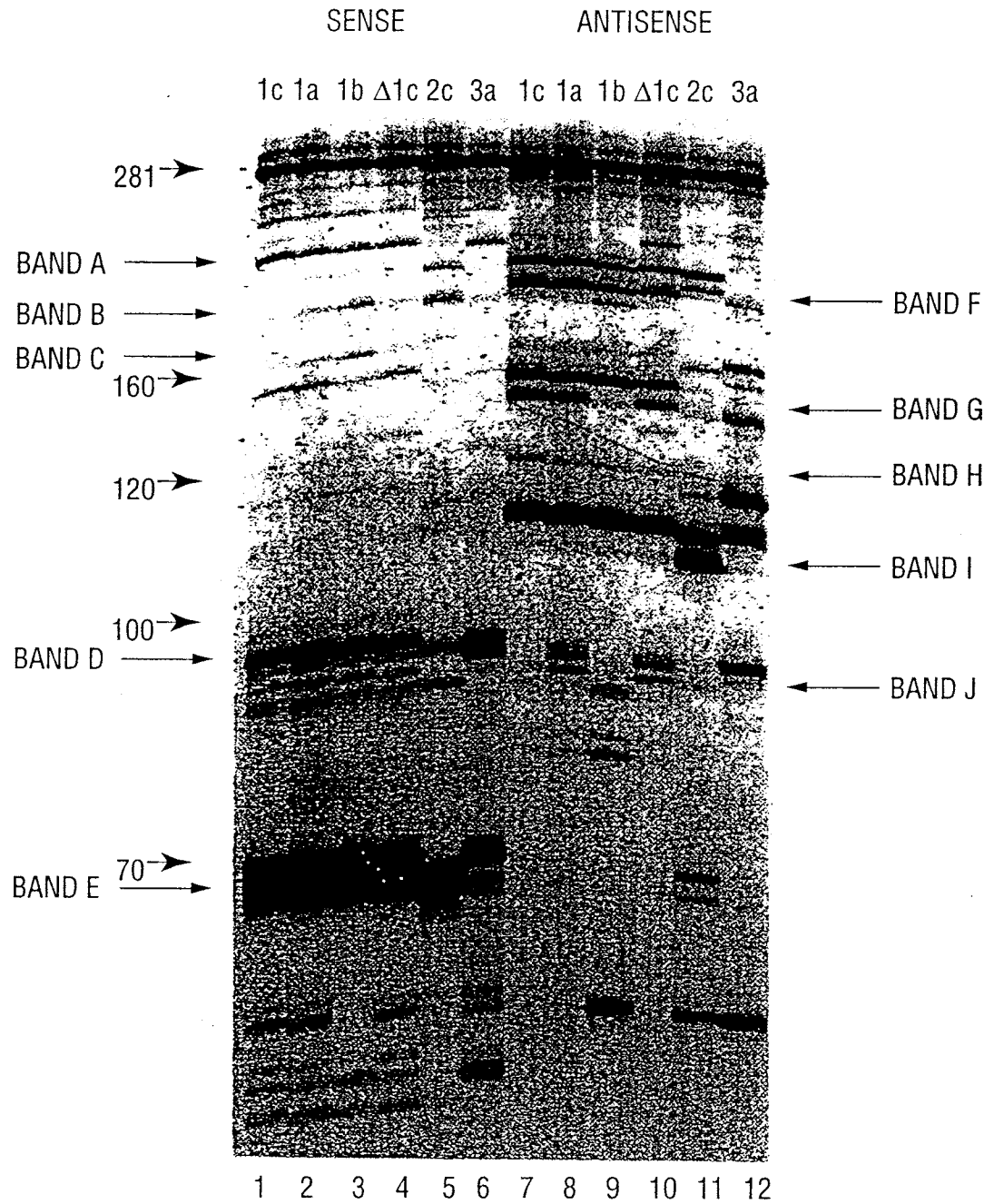
**FIG. 81**

FIG. 82

HCV1.1	(SEQ ID NO:121)	1	CTGTCTTAC	GCAGAAAGCG	TCTGGCCATG	GCCTTAGTAT	GAGTGTGCGT	50
HCV2.1	(SEQ ID NO:122)		CTGTCTTAC	GCAGAAAGCG	TCTAGCCATG	GCCTTAGTAT	GAGTGTGCGT	
HCV3.1	(SEQ ID NO:123)		CTGTCTTAC	GCAGAAAGCG	TCTAGCCATG	GCCTTAGTAT	GAGTGTGCGT	
HCV4.2	(SEQ ID NO:124)		CTGTCTTAC	GCAGAAAGCG	TCTAGCCATG	GCCTTAGTAT	GAGTGTGCGT	
HCV6.1	(SEQ ID NO:125)		CTGTCTTAC	GCAGAAAGCG	TCTAGCCATG	GCCTTAGTAT	GAGTGTGCGT	
HCV7.1	(SEQ ID NO:126)		CTGTCTTAC	GCAGAAAGCG	TCTAGCCATG	GCCTTAGTAT	GAGTGTGCGT	
HCV1.1		51	CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	100
HCV2.1			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV3.1			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV4.2			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV6.1			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV7.1			CAGCCTCCAG	GACCCCCCCT	CCCGGGAGAG	CCATAGTGGT	CTGCGGAACC	
HCV1.1		101	GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-AAA	150
HCV2.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV4.2			GGTGAGTACA	CCGGAATTGC	CAGGACGACC	GGTCCCTTTC	GGTGGATGTA	
HCV6.1			GGTGAGTACA	CCGGAATTGC	CGGGAAGACT	GGTCCCTTTC	TTGGAT-AAA	
HCV7.1			GGTGAGTACA	CCGGAATCGC	TGGGTGACC	GGTCCCTTTC	TTGGAT-CAA	
HCV1.1		151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCGAGA	CTGCTAGCCG	
HCV4.2			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1			CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1			CCCGCTCAAT	ACCCAGAAAT	TTGGGCGTGC	CCCCGCGAGA	TCACTAGCCG	
HCV1.1		201	AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	250
HCV2.1			AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	
HCV3.1			AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	
HCV4.2			AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	
HCV6.1			AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	
HCV7.1			AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCTGA	TAGGGTGCTT	
HCV1.1		251	GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1			GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV3.1			GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV4.2			GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV6.1			GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV7.1			GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		

**FIG. 83**

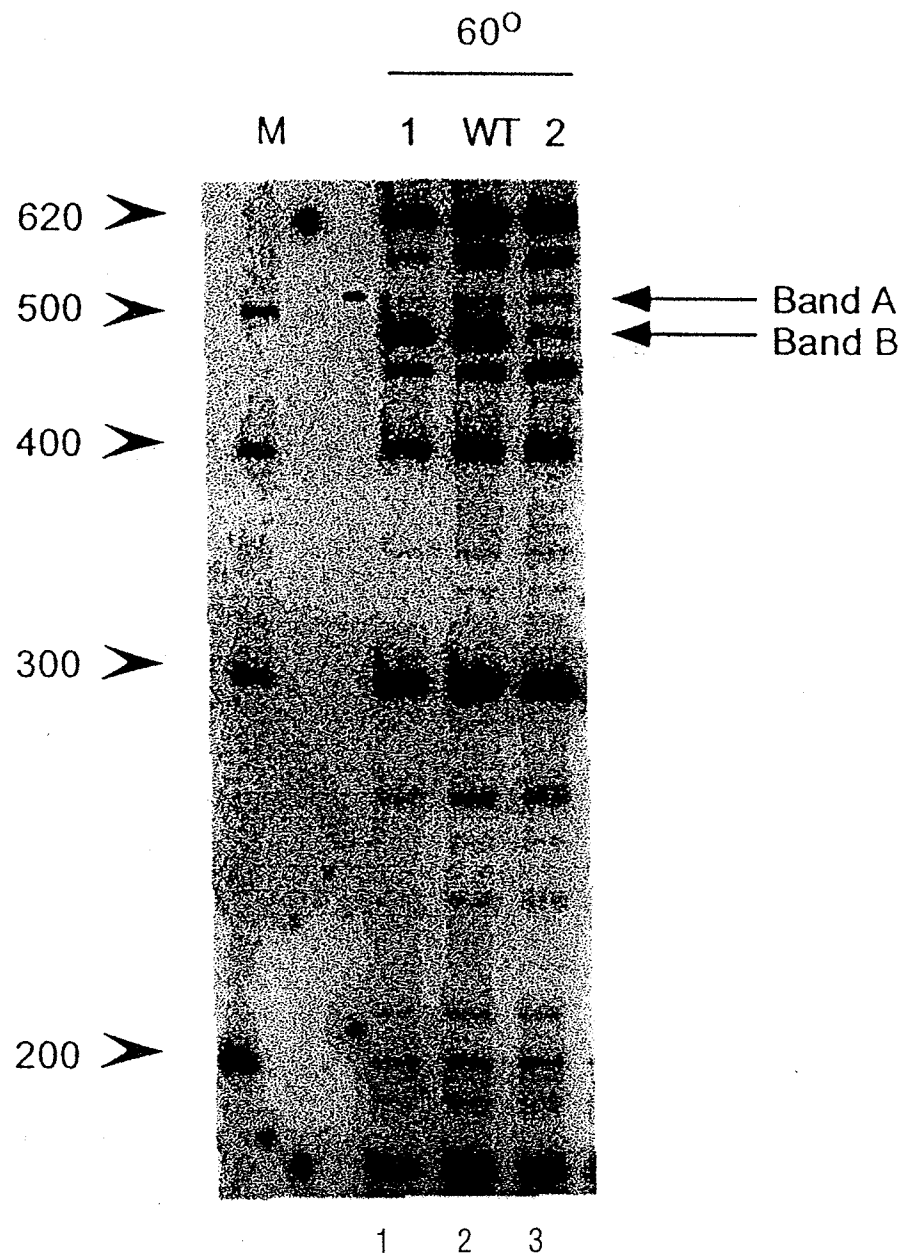


FIG. 84

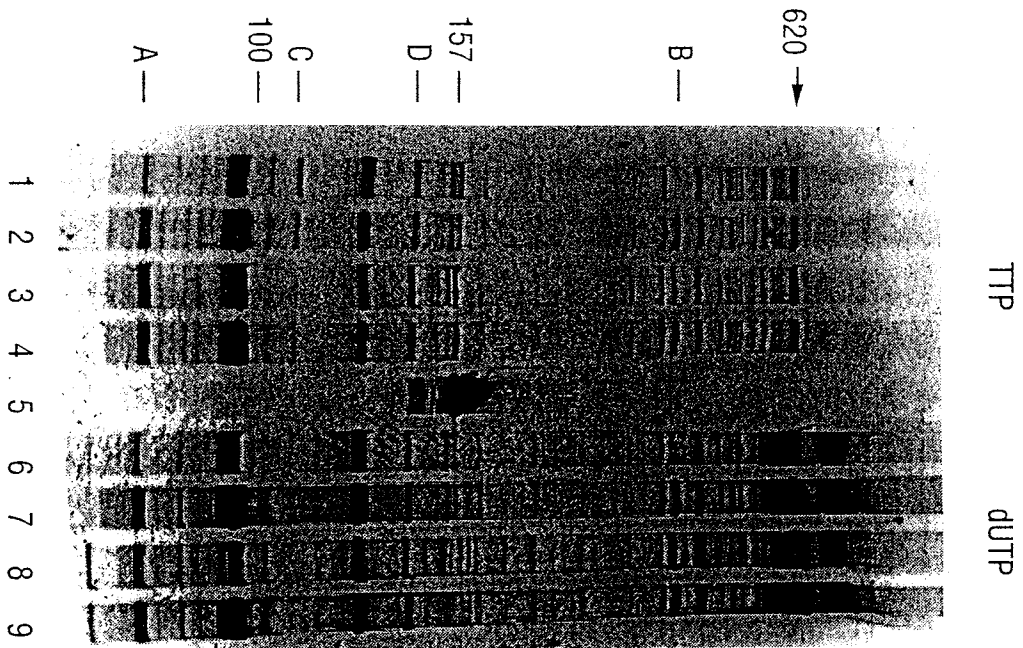


FIG. 85A

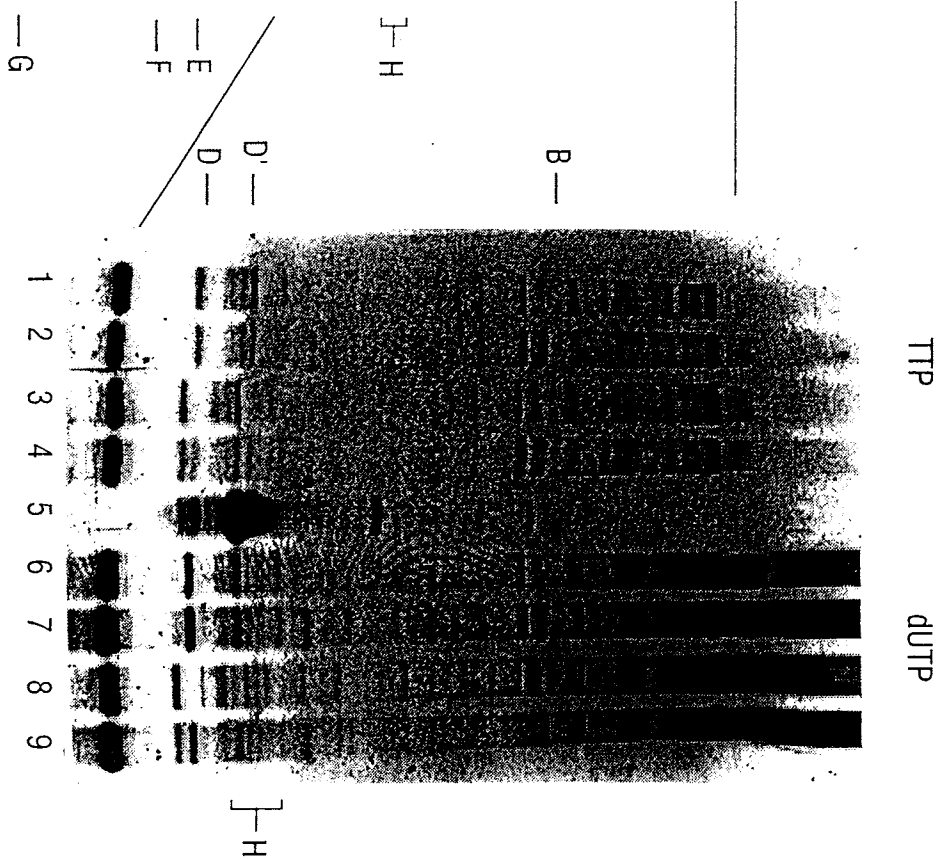


FIG. 85B

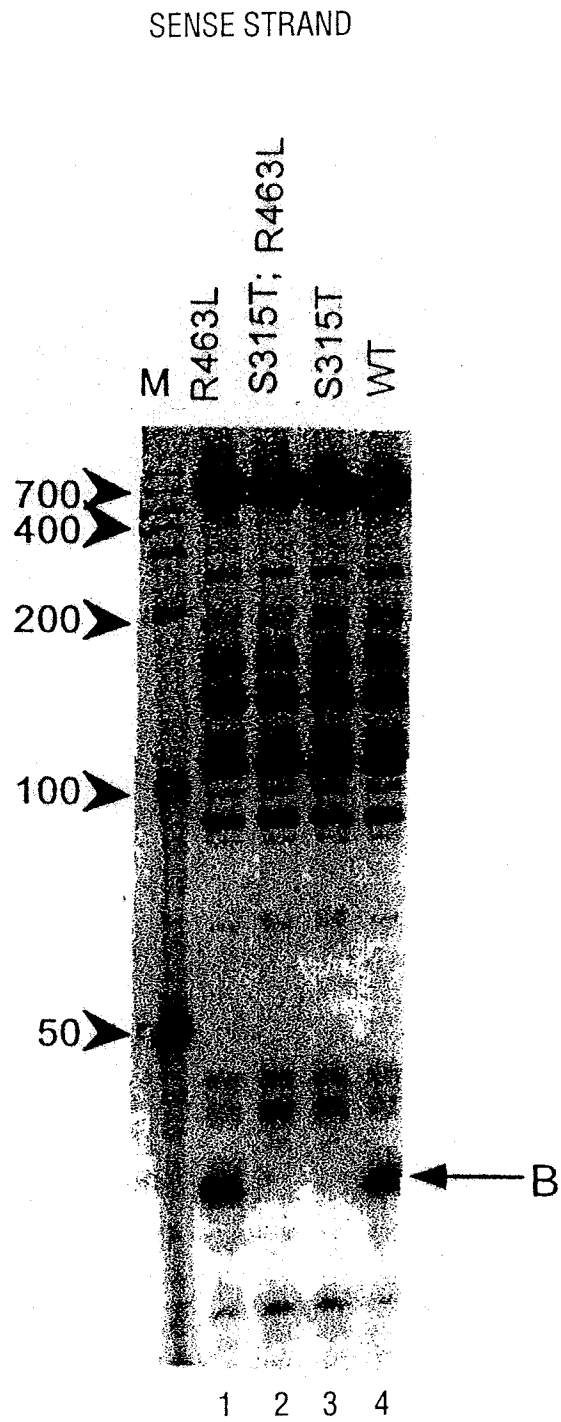
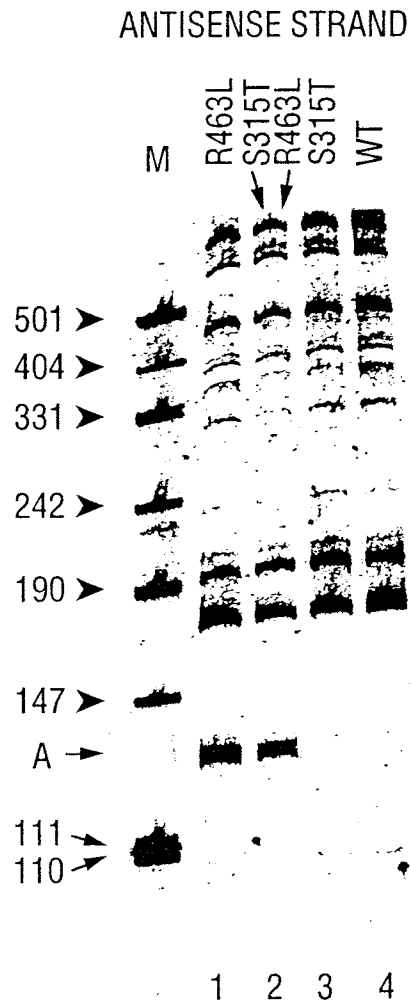


FIG. 86

**FIG. 87**

AGA GTTGTATCCT GGCTCAG	10	20	30	40	50	60	
AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCCTA ACACATGCCAA							1638
TTTAACCTCT CAAACTAGTA CCGAGTCTAA CTTGGCAGCCG CCGTCCGGAT TGTGTACGTT							
GTGGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGGGAC GGGTGAAGTAA	70	80	90	100	110	120	
CAGCTTGCCA TTGTCCTTCT TCGAACGAAG AAACGACTGC TCACCGCCTG CCCACTCAAT							ER10
TGTCTGGGAA ACTGCCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT	130	140	150	160	170	180	
ACAGACCCTT TGACGGACTA CCTCCCCCTA TTGATGACCT TTGCCATCGA TTATGGCGTA							
AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAAGATG	190	200	210	220	230	240	
TTGCAGCGTT CTGGTTTCTC CCCCTGGAAAG CCCGGAGAAC GGTAGCCTAC ACGGGTCTAC							
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGGGAC GATCCCTAGC TGGTCTGAGA	250	260	270	280	290	300	
CCTAATCGAT CATCCACCCC ATTGCCGAGT GGATCCGCTG CTAGGGATCG ACCAGACTCT							
GGATGACCCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG	310	320	330	340	350	360	
CCTACTGGTC GGTGTGACCT TGACTCTGTG CCAAGGTCTGA GGATGGCCCTC CGTGTGTC							1659

FIG. 88A

370	380	390	400	410	420
GGAATATTGC	ACCAATGGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGATG	AAGAAGGCCCT
CCTTATAACG	TGTTACCCCGC	GTTCCGACTA	CGTCGGTACG	GGGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGAGTAA	AGTTAATACC	TTTGCTCAAT
AGCCCAACAT	TTCATGAAG	TCGCCCCCTCC	TTCCCTCAT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGGCGGTT	TGTTAAGTCA
CCACGTTCCG	AATTAGCCTT	AATGACCCGC	ATTTCGCGTG	CGTCCGCCAA	ACAAATTCACT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCCGAG	TTGGACCCCT	GACGTAAGACT	ATGACCCGTT	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACCTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GGGGCCCCCT	GGACGGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCG	CACCCCTCGT

FIG. 88B

790	800	810	820	830	840
AACAGGATTA	GATACCCCTGG	TAGTCCACGC	CGTAAACGAT	GTCCGACTTG	AGGTTGTGCC
TTGTCCTAAT	CTATGGGACC	ATCAGGTGCG	GCATTGTGCTA	CAGCTGAACC	TCCAACACGG
850	860	870	880	890	900
CTTGAGGCGT	GGCTTCCGGA	GCTAACGCGT	TAAGTCGACC	GCCCTGGGGAG	TACGGCCGCA
GAACTCCCGCA	CCGAAGGCCCT	CGATTGCGCA	ATTCAGCTGG	CGGACCCCTC	ATGCCGGCGT
910	920	930	940	950	960
AGGTAAAAAC	TCAAATGAAT	TGACGGGGGGC	CCGCACAAGC	GGTGAGGCAT	GTGGTTTAAT
TCCAATTTTG	AGTTTACTTA	ACTGCCCCCGG	GGCGTGTTG	CCACCTCGTA	CACCAAATTA
970	980	990	1000	1010	1020
TCGATGCAAC	GGGAAGAACC	TTACCTGGTC	TTGACATCCA	CGGAAGTTT	CAGAGATGAG
AGCTACGTTG	CGCTTCTTGG	AATGGACCAG	AACTGTAGGT	GCCTTCAAAA	GTCCTTACTC
1030	1040	1050	1060	1070	1080
AAATGTGCCCTT	CGGGAACCGT	GAGACAGGTG	CTGCATGGCT	GTCGTCAGCT	CGTGTGTGTA
TTACACGGGAA	GCCCTTGGA	CTCTGTCCAC	GACGTACC	CAACAGTCCA	GCACAACACT
1090	1100	1110	1120	1130	1140
	GC	AACGAGCGCA	ACCC		
1150	1160	1170	1180	1190	1200
AAATGTTGGGT	TAAGTCCCGC	AACGAGCGCA	ACCCCTTATCC	TTTGTGCGCA	GGGGTCCGGC
TTACAACCCA	ATTCAGGGCG	TTGCTCGCGT	TGGGAATAGG	AAACAACGGT	CGCCAGGCCG
				ATG	ACGTCAAGTC
				ATG	ACGTCAAGTC
CGGGAAGTCA	AAGGAGACTG	CCAGTGATAA	ACTGGAGGAA	GGTGGGGATG	ACGTCAAGTC
GCCCTTGAGT	TTCCTCTGAC	GGTCACTATT	TGACCTCCTT	CCACCCCTAC	TGCAGTTTCA

FIG. 88C

SB-1

SB-3
SB-4

1210 1220 1230 1240 1250 1260
 ATCATGGCCC TTA
 ATCATGGCCC TTACGA
 ATCATGGCCC TTACGA
 TAGTACCAGG AATGCTGCTC
 SB-3
 SB-4

1270 1280 1290 1300 1310 1320
 ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TCGCTCGTAG TCCGGATTGG AGTCTGCAAC
 TGAGGCGCTC TCGTTCGCC TGGAGTATTTC ACGCAGCATC AGGCCTAACC TCAGACGTTG
 1330 1340 1350 1360 1370 1380
 TC GACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT
 AGCTGAGGTA CTTCAAGCCTT AGCGATCATT AGCACCCTAGT CTTACGGTGC CACTTAATGCA
 GC CACTTATGCA
 1743

1390 1400 1410 1420 1430 1440
 TCCCCGGGCT TGTACACACACC GCCCGTCACA CCATGGGAGT GGGTTGCCAA AGAAGTAGGT
 AGGGCCCCGGA ACATGTGTGG CGGGCAGTGT GGTACCCCTCA CCCAACGTTT TCTTCATCCA
 AGGGCCCCGGA ACATG
 1743

1450 1460 1470 1480 1490 1500
 AGCTTAACCT TCGGGAGGGC GCTTACCACCT TTGTGATTCA TGACTGGGGT GAAGTCGTAA
 TCGAATTGGA AGCCCTCCCG CGAATGGTGA AACACTAAGT ACTGACCCCA CTTCAAGCATT
 1510 1520 1530 1540 1550
 CAAGGTAACC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA.....
 GTTCCATTGG CATCCCTTGG GACGCCAACCT TAGTGGAAGGA AT.....

FIG. 88D

```

1638 (SEQ ID NO:151)      AGAGTTTGATCCTGGCTCAG
E.colirre(SEQ ID NO:158)0 ..AAATTGAAGAGTTTGTATCATGGCTCAGATTGAACGCTGGCGGCAGGCCCTAACACATGCA
Cam.jejun5(SEQ ID NO:159)0 ~TTTTATGAGAGTTTGTATCCTGGCTCAGAGTGAACGCTGGCGGCCTGCTTAATACATGCA
Stp.aureus(SEQ ID NO:160)0 ..TTTTATGAGAGTTTGTATCCTGGCTCAGGATGAACGCTGGCGGCCTGCTTAATACATGCA

ER10 (SEQ ID NO:152)      GCGGACGGG
E.colirre
Cam.jejun5
Stp.aureus
60 AGTCGAACGGTAACAG----GAAGAAAGCTTGCTTCTTT----GCTGACGAGTGGCGGACGGG
62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAAGTGA-----TTAGTGGCGCACGGG
61 AGTCGAGCGAA-----CGGACGAGAAAGCTTGCTTCTCTGATG----TT-AGCGGCGGACGGG

ER10
E.colirre
Cam.jejun5
Stp.aureus
114 TGAGTAATGTCTGGGA-AACTGCCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATA
114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAAGAGGACAAACAGTTGGAACGACTGCTAATA
113 TGAGTAACACAGTGATTAACCTAACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATA
      TGAGTAA
E.colirre
Cam.jejun5
Stp.aureus
175 CCGCATAAC-----GTGCAAGAC-----CAAAGAGGGGGACCTTCG-GGCCCTTG
176 CTCTATACCTCCTGCTTAACACAAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
175 CCGGATAATATATTTGAACCGCATGTTCAAAAGTGAAAGACGGT----CTT----GCTGTCA

E.colirre
Cam.jejun5
Stp.aureus
221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTAGGTGGGTAACGGCTCACCTAAGCGGACGA
221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA

E.colirre
Cam.jejun5
Stp.aureus
283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACCTGAGACACAGGTCAGACTCCTA
283 CGCTTAACCTGGTCTGAGAGGATGATCAGTCACACTGGAACCTGAGACACAGGTCAGACTCCTA
291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACCTGAGACACAGGTCAGACTCCTA
      ACTCCTA
1659 (COMPL)

```

FIG. 89A

E.colirrsE
Cam.jejun5
Stp.aureus
1659(COMPL)

345 CGGAGGCCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTG
345 CGGAGGCCAGCAGTAGGGAATATTGCCAATGGGGGAAACCCCTGACGCAACGCGCGTG
353 CGGAGGCCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAACGCGCGGTG
CGGAGGCCAGCAG

E.colirrsE
Cam.jejun5
Stp.aureus

407 TATGAAGAAAGCCCTTCGGGTTGTAAAGTACTTTCAAGCGGGAGGAA-GGAGTAAAGTTAAT
407 GAGATGACACTTTTCGGAGCGTAACCTCCTTTCTTAGGGAA------AATT
415 AGTATGAAGTCTTCGGATCGTAAACTCTGTATTAGGGAAGACATATGTGTAAGTAAC

E.colirrsE
Cam.jejun5
Stp.aureus

468 ACCTTTGCTCATTGACGTTACCCGCAAGAAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
455 C------TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
476 -TGTGCACATCTTGACCGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG

FIG. 89B

E. coli rrSE	530	GTAATACGGAGGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAGCGGCACGCGAGGCGGTTT
Cam. jejuns	506	GTAATACGGAGGGGTGCAAGCGTTACTCGGAATCACTGGGCGTAAGGCGCGTAGGCGGATT
Stp. aureus	538	GTAATACGTAAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAGCGCGCGTAGGCGGTTT
E. coli rrSE	592	GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACCTGCATCTGATACTGGCAAGCTT
Cam. jejuns	568	ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAACCTGCTTGGAACCTGATAGTCTA
Stp. aureus	600	TTTAAGTCTGATGTGAAAGCCACGGCTCAACCGTGGAAGGTCATTGGAAACTGGAAAACTT
E. coli rrSE	654	GAGTCTCGTAGAGGGGGTAGAATTCCAGGTGTAGCGGTGAATGCCGTAGAGATCTGGAGGA
Cam. jejuns	630	GAGTGAGGGAGAGGCGAGATGGAATTGGTGGTAGGGGTAAATCCGTAGATATCACCAAGA
Stp. aureus	662	GAGTGCGAAGAGAGGAAAGTGGAATCCATGTGTAGCGGTGAAATGCCGAGAGATATGGAGGA
E. coli rrSE	716	ATACCGGTGGCGAAGGCGGCCCCCTGGACGGAAGACTGACCGCTCAGGTGCGAAAGCGTGGGGA
Cam. jejuns	692	ATACCCCATTTGCCGAAGGCGATCTGCTGGAACCTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp. aureus	724	ACACCAAGTGCGGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCCAAAGCGTGGGGA
E. coli rrSE	778	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCGGTAAACGATGTCGACTTGAGGTTGTGC
Cam. jejuns	754	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCGCTAAACGATGTACACTAGTTGTTGGGGT
Stp. aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCGCGTAAACGATGAGTGCTAAGTGTAGGGG

FIG. 89C

E. coli irse	840	C-CTTGA-GGCGTGCTTCCGGAGCTAACGGGTTAAGTCGACCCGCTGGGGAGTACGGCCG
Cam. jejuns	816	G-CTAGT-CATCTCAGTAATGACGCTAACGCATTAAAGTGTACCGCTGGGGAGTACGGTCG
Stp. aureus	848	GT-TTCCGCCCCCTTAGTGTGCTGCAGCTAACGCATTAAAGCACTCCGCTGGGGAGTACGACCG
E. coli irse	900	AAGGTTAAAACTCAAATGAATTGACGGGGGGCCCGCACAAAGCGGTGGAGCATGTGGTTAATT
Cam. jejuns	876	AAGATTAAAACTCAAAGGAATAGACGGGGGACCCGCACAAGCGGTGGAGCATGTGGTTAATT
Stp. aureus	909	AAGGTTGAAACTCAAAGGAATTGACGGGGGACCCGCACAAGCGGTGGAGCATGTGGTTAATT
E. coli irse	962	CGATGCCAACGGCGAAGAACCCTTACCTGGTCTTGACATCCACGGGAAGTTTTCAGAGATGAGAAT
Cam. jejuns	938	CGAAGATACGGCGAAGAACCCTTACCTGGGCTTGATATCCTAAGAACCCTTTCAGAGATAAGAGG
Stp. aureus	971	CGAAGCAACGGCGAAGAACCCTTACCAATCTTGACATCCTTTGACCAACTCTAGAGATAGAGCC
E. coli irse	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCGTCAGCTCGTGTGTGA
Cam. jejuns	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTCAGCTCGTGTGTGA
Stp. aureus	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGCTGCATGCTGTCGTCAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
E. coli irse	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTATCCTTTGTTGCCAGCGGTCGGG-CC
Cam. jejuns	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTAATTAGTTGCTAACGGTTCGG-CC
Stp. aureus	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

FIG. 89D

SB-3 (SEQ ID NO:157)		ATGACGTCAGTCATC
SB-4 (SEQ ID NO:154)		ATGACGTCAGTCATC
E.colirrsE	1142	GGGAACCTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACGTCAGTCATC
Cam.jejuns	1122	GAGCACTCTAAATAGACTGCCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAGTCATC
Stp.aureus	1152	GGGCACTCTAAGTTGACTGCCGGTGACCAAAACCGGAGGAAGGTGGGGATGACGTCAAATCATC
SB-3		ATGGCCCTTA
SB-4		ATGGCCCTTACGA
E.colirrsE	1204	ATGGCCCTTACGACCAGGGCTACACACGCTGCTACCAATGGCGCATACAAAGAGAAGCGACCTC
Cam.jejuns	1183	ATGGCCCTTATGCCCAGGGCGACACACGCTGCTACCAATGGCATATAGAAATGAGACGCAATACC
Stp.aureus	1214	ATGCCCTTATGATTGGGCTACACACGCTGCTACCAATGGACAATAACAAAGGGCAGCGAAACC
E.colirrsE	1266	GCAGAGGCAAGCGGACCTCATAAAGTGCGTCTAGTCCGGATTGGAGTCTGCCAATCTGACTC
Cam.jejuns	1245	GCAGAGGTGGAG-CAAATCTATAAAATATGTCCGAGTTCCGATTGTTCTCTGCAACTCGAGAG
Stp.aureus	1276	GCAGAGGTCAAGCAAAATCCCATAAAGTTGTTCTCAGTTCCGATTGTAGTCTGCAACTCGACTA
E.colirrsE	1328	CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam.jejuns	1306	CATGAAGCCGGAAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp.aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743(compl)		CGGTGAATACGTTCCCGGGC

FIG. 89E

```
E.coli rrse 1389 CTTGTACACACCCGCCCGTCACACCAATGGGAGTGGGTTGCCAAAGAAGTAGGTAACCT
Cam. jejuns 1368 CTTGTACTCACC GCCCGCTCACACCAATGGGAGTTGATTTCACCTCGAAGCCGGAATACT--A-A
Stp. aureus 1399 ATTGTACACACCCGCCCGTCACACCAAGAGTTTGTAAACACCCGAAGCCGGTGAGTAACCT
1743 (compl) CTTGTAC

E.coli rrse 1451 TCG_gGAGGGCGCTTACCACCTTTGTGATTCATGACTGGGGTGAAAGTCGTAACAAGGTAACCG
Cam. jejuns 1427 AC--T-AGTTACCGTCCACAGTGGAAATCAGCGACTGGGGTGAAAGTCGTAACAAGGTAACCG
Stp. aureus 1461 TTAGGAGCTAGCCGTCGAAGGTGGGACCAATGATTGGGGTGAAAGTCGTAACAAGGTAAGCCG

E.coli rrse 1512 TAGGGGAACCTGGCGGTGGATCACCTCCTTA---
Cam. jejuns 1485 TAGGAGAACCCTGGCGGTGGATCACCTCCT----
Stp. aureus 1523 TATCGGAAGGTGCGGCTGGATCACCTCCTTTCT-
```

FIG. 89F

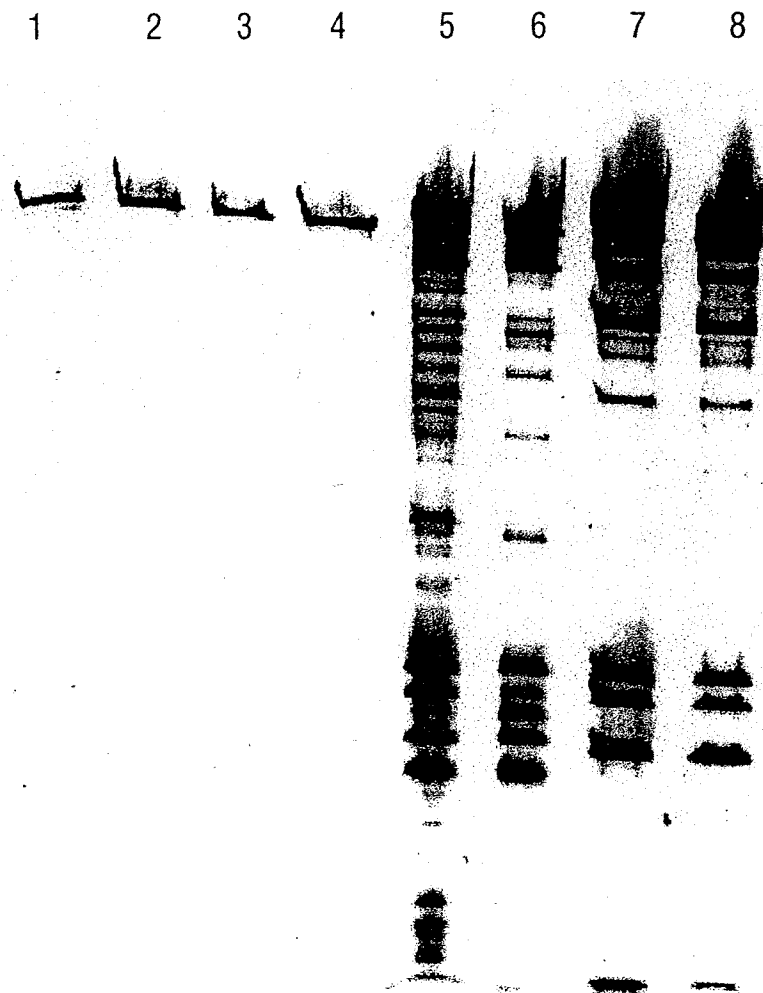


FIG. 90

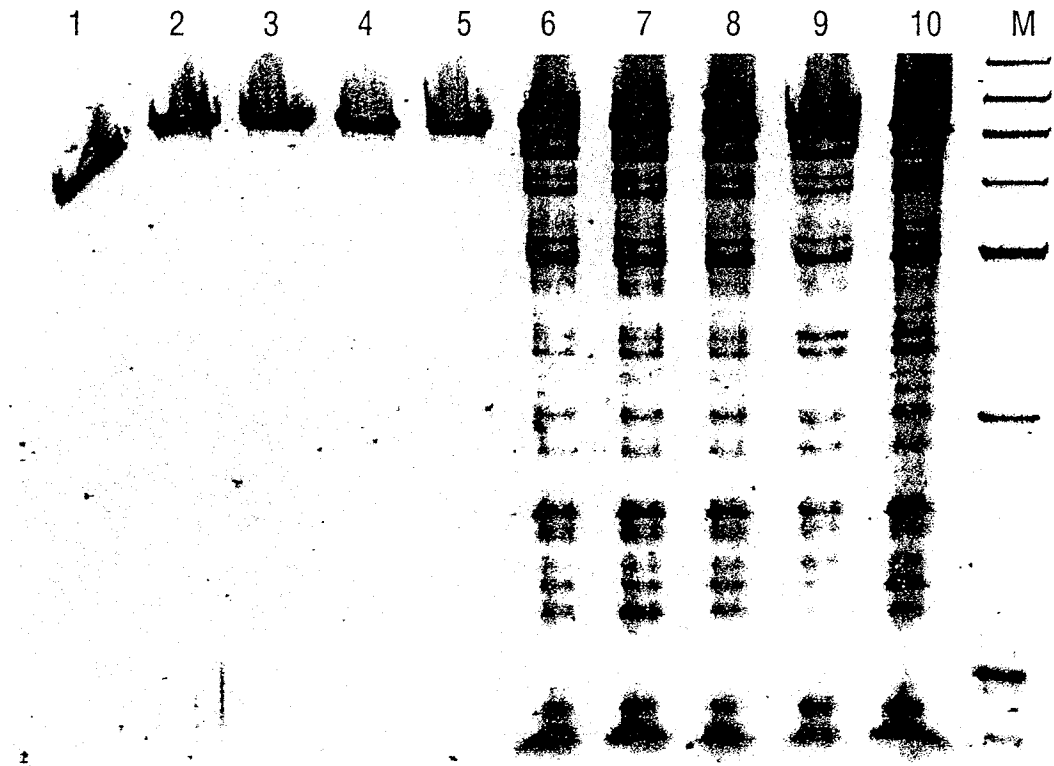


FIG. 91A

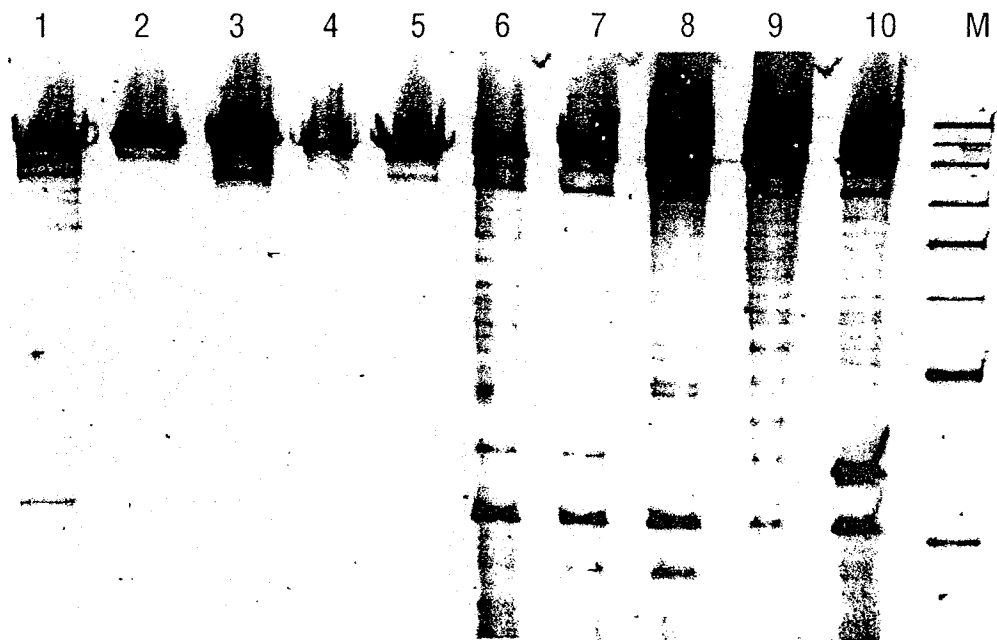


FIG. 91B

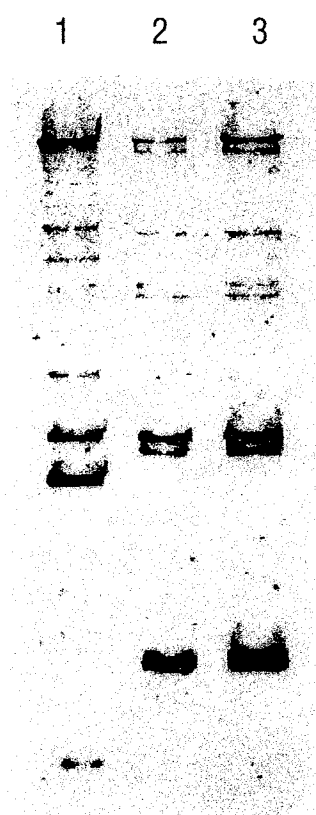


FIG. 92

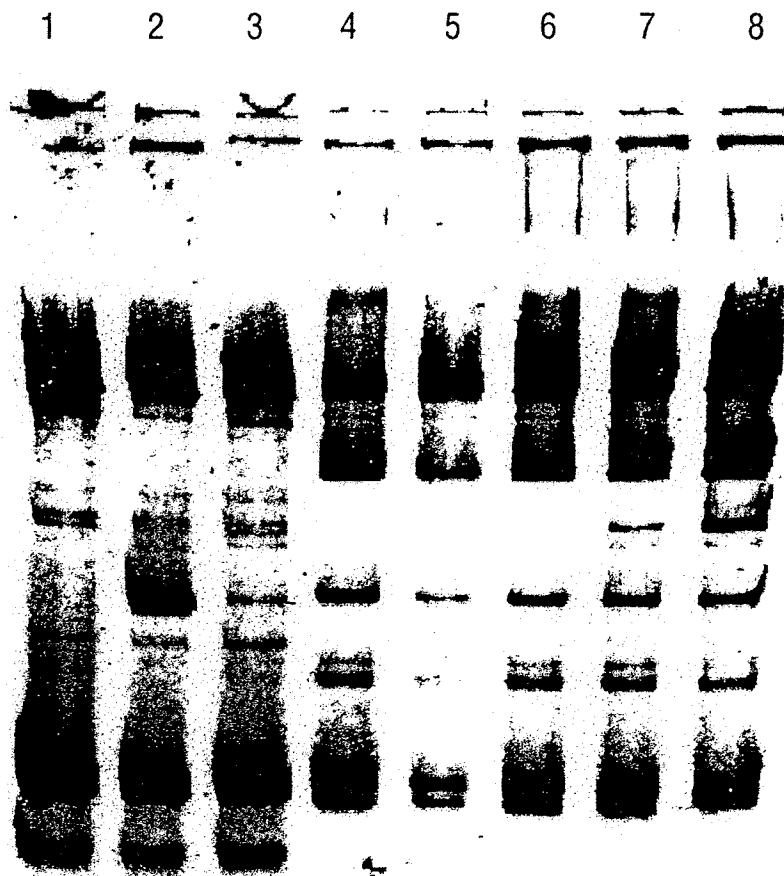


FIG. 93

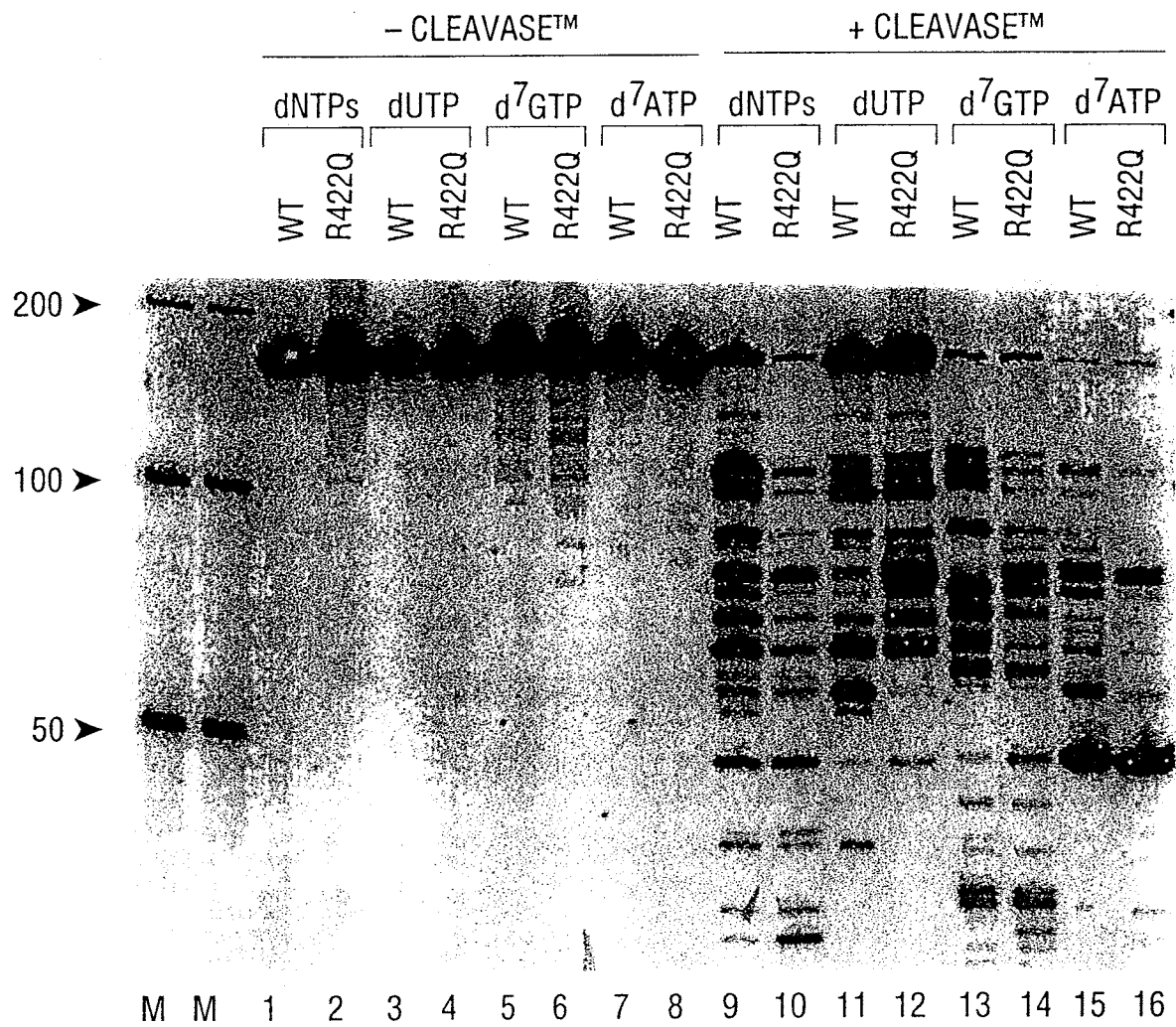


FIG. 94